

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 11858.6 Seconds
(without alignments)
10957.506 Million cell updates/sec

Title: US-10-728-051-1

Perfect score: 2032

Sequence: 1 aataatcatatattcatc.....cgttgtgcgtgttctcc 2032

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_env.*

2: gb_pat.*

3: gb_ph.*

4: gb_pl.*

5: gb_pr.*

6: gb_ro.*

7: gb_sts.*

8: gb_sy.*

9: gb_un.*

10: gb_vi.*

11: gb_ov.*

12: gb_htg.*

13: gb_in.*

14: gb_om.*

15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2032	100.0	2032	2	AR257469 Sequence
2	2032	100.0	2032	2	AR629098 Sequence
3	2032	100.0	2032	2	AR716329 Sequence
4	2032	100.0	2032	2	AX148742 Sequence
5	2032	100.0	2032	4	ARQARAH1 L34402 Arachis hyp
6	2032	100.0	2041	2	AR257470 Sequence
7	2019.2	99.4	2032	2	AX155331 Sequence
8	1930	95.0	1930	2	BD107898 Methods a
9	1930	95.0	1930	2	BD172109 Peanut al
10	1930	95.0	1930	2	AR257463 Sequence
11	1805.2	88.8	1978	2	AX155332 Sequence
12	1752.4	86.2	1949	2	AR257467 Sequence
13	1752.4	86.2	1949	2	AR629097 Sequence
14	1752.4	86.2	1949	4	ARQARAH L38853 Arachis hyp
15	1608	79.1	2674	4	AF432231 Arachis h
16	1395.4	68.7	2332	4	AY581852 Arachis h
17	1375.4	67.7	1418	4	AY581851 Arachis h
18	954.4	47.0	1035	4	AY581850 Arachis h

19	891.2	43.9	1047	4	AY581849	AY581849 Arachis h
20	750	36.9	750	2	AR257466	AR257466 Sequence
21	468.6	23.1	1257	4	LCU551424	AJ551424 Lens culi
22	465.8	22.9	1433	4	PSVIC	Y00722 Pisum sativ
23	461	22.7	1561	4	VFVIC	Y00462 Vicia faba
24	455.4	22.4	1248	4	LCU551425	AJ551425 Lens culi
25	449	22.1	1248	4	AJ626897	AJ626897 Pisum sat
26	449	22.1	1596	4	PSVICK	X67429 Pisum sativ
27	446	21.9	1791	4	AY500372	AY500372 Lupinus a
28	444.2	21.9	1248	4	AJ626898	AJ626898 Pisum sat
29	435.4	21.4	1548	4	VNVICLN	Z71987 V narbonens
30	408.4	20.1	1251	4	AB008679	AB008679 Glycine m
31	408.4	20.1	1350	2	AR714521	AR714521 Sequence
32	408.4	20.1	1412	4	AB197786	AB197786 Glycine m
33	408.4	20.1	3808	2	AR714525	AR714525 Sequence
34	408.4	20.1	3808	2	AR714526	AR714526 Sequence
35	406.8	20.0	1254	2	AR714452	AR714452 Sequence
36	406.8	20.0	1278	2	AR714451	AR714451 Sequence
37	406.8	20.0	1320	2	BD175903	BD175903 Regulatio
38	406.8	20.0	1320	2	AR202568	AR202568 Sequence
39	406.8	20.0	1320	2	AR486455	AR486455 Sequence
40	406.8	20.0	1320	2	AR615272	AR615272 Sequence
41	406.8	20.0	1320	2	AR714443	AR714443 Sequence
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43	404	19.9	1818	2	BD175901	BD175901 Regulatio
44	404	19.9	1818	2	AR202566	AR202566 Sequence
45	404	19.9	1818	2	AR486453	AR486453 Sequence

ALIGNMENTS

RESULT 1
AR257469
LOCUS AR257469 2032 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 21 from patent US 6486311.
ACCESSION AR257469
VERSION AR257469.1 GI:27307482
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2032)
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,
Helm,R.M. and Bannon,G.A.
TITLE Peanut allergens and methods
JOURNAL Patent: US 6486311-A 21 26-NOV-2002;
NY Mc. Sinai School of Medicine and University of Arkansas; New York,

FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 2032; DB 2; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGGGAG 60
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Db 61 GGTTTCTCCACTGATGCTGTGTAGGGATCCTTGTCTGGCTTCAGTTTCTGCAACGCA 120
Qy 121 TGCCAAGTCATCACCTTACAGAGAAAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
Db 121 TGCCAAGTCATCACCTTACAGAGAAAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
Qy 181 GAGTTCTCAACAGGACCGGATGACTTGAGCAAAAGGCGATGCGAGTCTCGCTGCACCAA 240

Db	181	GAGTTGTAAACAGGAACCGGATGACTTTGAAGCAAAAAGGCATGCGAGTCTCGCTGCACCAA	240
Qy	241	GCTCGAGTATGATCCTCGTTGTGCTATGATCTCGAGGACACACTGGCACCAACCAACCA	300
Db	241	GCTCGAGTATGATCCTCGTTGTGCTATGATCTCGAGGACACACTGGCACCAACCAACCA	300
Qy	301	AGCTTCCCTCCAGGGGAGCGGACAGCTGGCCGCCAACCCGGAGACTACGATGATGACCG	360
Db	301	ACGTTCCCTCCAGGGGAGCGGACAGCTGGCCGCCAACCCGGAGACTACGATGATGACCG	360
Qy	361	CCGTCAACCCCGAAGAGAGAGGAGCGGATGCGGACACAGCTGGACCCGAGGGAGCGTGA	420
Db	361	CCGTCAACCCCGAAGAGAGAGGAGCGGATGCGGACACAGCTGGACCCGAGGGAGCGTGA	420
Qy	421	AAGAGAAGAGACTGGAGACAACCAAGAGAGAAGATTGGAGGCGACCAAGTCAATCAGCAGCC	480
Db	421	AAGAGAAGAGACTGGAGACAACCAAGAGAGAAGATTGGAGGCGACCAAGTCAATCAGCAGCC	480
Qy	481	ACGGAATAAGGCCCGAAGGAAGAGAGAGAAAGAGTGGGGAACACCAGGTAGCCA	540
Db	481	ACGGAATAAAGGCCCGAAGGAAGAGAGAGAAAGAGTGGGGAACACCAGGTAGCCA	540
Qy	541	TGTGAGGGAAGAAACATCTCGGAACCAACCTTTCTACTTCCCGTCAAGGGCGTTTAGCAC	600
Db	541	TGTGAGGGAAGAAACATCTCGGAACCAACCTTTCTACTTCCCGTCAAGGGCGTTTAGCAC	600
Qy	601	CCGCTACGGGAACCAAAAACGGTAGGATCGGGTCTCGAGAGTTTGAACAAAAGGTCAAG	660
Db	601	CCGCTACGGGAACCAAAAACGGTAGGATCGGGTCTCGAGAGTTTGAACAAAAGGTCAAG	660
Qy	661	GCAGTTTCAGAACTCCAGAAATCACCGTATGTGCGAGATCGAGGCCAACAACCTCAACTCT	720
Db	661	GCAGTTTCAGAACTCCAGAAATCACCGTATGTGCGAGATCGAGGCCAACAACCTCAACTCT	720
Qy	721	TGTTCTTCCCAACGACGCTGATGCTGATAACATCTTGTGTTATCCAGCAAGGGCAAGCCAC	780
Db	721	TGTTCTTCCCAACGACGCTGATGCTGATAACATCTTGTGTTATCCAGCAAGGGCAAGCCAC	780
Qy	781	CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTTGACGAGGGCCATGCAT	840
Db	781	CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAATCTTTGACGAGGGCCATGCAT	840
Qy	841	CAGAAATCCCATCGGTTTCAATCTTCTACATCTTGAACCCGCATGACAAACAGAACTCTAG	900
Db	841	CAGAAATCCCATCGGTTTCAATCTTCTACATCTTGAACCCGCATGACAAACAGAACTCTAG	900
Qy	901	AGTAGCTAAAATCTCCATGCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC	960
Db	901	AGTAGCTAAAATCTCCATGCCCGTTAACACACCCGGCCAGTTTGAGGATTTCTTCCCGGC	960
Qy	961	GAGCAGCCGAGACAATCATCTTCTGACGGGCTTCAGCAGGAATACTGTTGAGGCGGC	1020
Db	961	GAGCAGCCGAGACAATCATCTTCTGACGGGCTTCAGCAGGAATACTGTTGAGGCGGC	1020
Qy	1021	CTTCAATCGGAATTCATCAGATACGAGGGTCTGTTAGAGAGAAATCAGAGAGTGA	1080
Db	1021	CTTCAATCGCGAATTCATCAGATACGAGGGTCTGTTAGAGAGAAATCAGAGAGTGA	1080
Qy	1081	GCAAGAGGAGAGGGCAGAGGGCATGAGTACTCGGAGTAGTGAGAAACAATGAAGAGT	1140
Db	1081	GCAAGAGGAGAGGGCAGAGGGCATGAGTACTCGGAGTAGTGAGAAACAATGAAGAGT	1140
Qy	1141	GATAGTCAAAAGTGTCAAAGAGACGTTTGAAGAACTTACTTAAGACGCTAAATCCGTTCTC	1200
Db	1141	GATAGTCAAAAGTGTCAAAGAGACGTTTGAAGAACTTACTTAAGACGCTAAATCCGTTCTC	1200
Qy	1201	AAAGAAAGGCTCCGAGAGAGGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGA	1260
Db	1201	AAAGAAAGGCTCCGAGAGAGGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGA	1260
Qy	1261	GCCCGATCTTTCTAAACAACTTTGGGAAGTATTTTGGGTGAAGCCAGACAAGAAAGACCC	1320
Db	1261	GCCCGATCTTTCTAAACAACTTTGGGAAGTATTTTGGGTGAAGCCAGACAAGAAAGACCC	1320

Qy	1321	CCAGCTTTCAGGACCTGGACATGATGATCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT	1380
Db	1321	CCAGCTTTCAGGACCTGGACATGATGATCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT	1380
Qy	1381	GCTCCACACTTCAACTCAAGGCCATGTTATCGTCTGTCGTCACAAAGGAACCTGAAA	1440
Db	1381	GCTCCACACTTCAACTCAAGGCCATGTTATCGTCTGTCGTCACAAAGGAACCTGAAA	1440
Qy	1441	CCTTGAATCTCGTGGCTGTAAAGAAAAGAGCAACAAAGAGGGGACGCGGGAAGAGGA	1500
Db	1441	CCTTGAATCTCGTGGCTGTAAAGAAAAGAGCAACAAAGAGGGGACGCGGGAAGAGGA	1500
Qy	1501	GGACGAAGACGGAAGAGAGGAGGAAGTAACAGAGAGGTGCGTAGTACACAGCGAGGTT	1560
Db	1501	GGACGAAGACGGAAGAGAGGAGGAAGTAACAGAGAGGTGCGTAGTACACAGCGAGGTT	1560
Qy	1561	GAGGAAGCGGATGCTTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC	1620
Db	1561	GAGGAAGCGGATGCTTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC	1620
Qy	1621	CGAACTCCATCTGCTTTGGCTTCGGTATCAACGCTGAAAAACAACCAAGAAATCTTCTTGC	1680
Db	1621	CGAACTCCATCTGCTTTGGCTTCGGTATCAACGCTGAAAAACAACCAAGAAATCTTCTTGC	1680
Qy	1681	AGTGATTAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATCCC	1740
Db	1681	AGTGATTAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATCCC	1740
Qy	1741	TGGTCCGGTGAACAAGTTTGAGAAAGCTCATCAAAAACCAAGAGAAATCTCACCTTGTGAG	1800
Db	1741	TGGTCCGGTGAACAAGTTTGAGAAAGCTCATCAAAAACCAAGAGAAATCTCACCTTGTGAG	1800
Qy	1801	TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT	1860
Db	1801	TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAAT	1860
Qy	1861	AGAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGCTCACTCTTCAATTTTGAAGGC	1920
Db	1861	AGAGGATCAAGAGGAGGAAAAACCAAGGAGGAGGCTCACTCTTCAATTTTGAAGGC	1920
Qy	1921	TTTTTAAGTGAAGTGGAGCAACTTGTATGATCGATAATTAAGATCAAGCTTTTGTACT	1980
Db	1921	TTTTTAAGTGAAGTGGAGCAACTTGTATGATCGATAATTAAGATCAAGCTTTTGTACT	1980
Qy	1981	CTACTATCAAAAACTTATCAATAAAAAAGCTTTGTGGTGTCTTCTCC	2032
Db	1981	CTACTATCAAAAACTTATCAATAAAAAAGCTTTGTGGTGTCTTCTCC	2032

RESULT 2

AR629098	AR629098	2032 bp	mRNA	linear	PAT 14-FEB-2005
LOCUS	Sequence 5 from patent US 6835824.				
DEFINITION	AR629098				
ACCESSION	AR629098.1				
VERSION	GI:59756573				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2032)				
AUTHORS	Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.				
TITLE	Peanut allergens and methods				
JOURNAL	Patent: US 6835824-A 5 28-DEC-2004;				
FEATURES	University of Arkansas; Little Rock, AR				
	Location/Qualifiers				
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	/mol_type="mRNA"				

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Query Match 100.0%; Score 2032; DB 2; Length 2032;

Best Local Similarity 100.0%; Pred. No. 0;		Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	AATATCATATATATTCATCAATCATCTATATATAGTAGCAGGAGCAATAGAGGGAG	60
Db	1	AATATCATATATATTCATCAATCATCTATATATAGTAGTAGCAGGAGCAATAGAGGGAG	60
Qy	61	GGTTCTCCACTGATGCTGTGTGTAGGATCCTTTGCTCCTGGCTTCAGTTTCTGCAACGCA	120
Db	61	GGTTCTCCACTGATGCTGTGTGTAGGATCCTTTGCTCCTGGCTTCAGTTTCTGCAACGCA	120
Qy	121	TGCCAGTCTACCTTACAGAGAAACAGAGAACCCCTGGCCAGAGGTGCCTCCA	180
Db	121	TGCCAGTCTACCTTACAGAGAAACAGAGAACCCCTGGCCAGAGGTGCCTCCA	180
Qy	181	GAGTTGTCAACAGGAAACCGATGACTTGAAGCAAAAGGCATGCGAGTCTCGCTGCACAA	240
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Qy	241	GCTCGATATGATCCTCGTTGTGTATGATCTCTCGAGGACACACTGGCACCAACCA	300
Db	241	GCTCGATATGATCCTCGTTGTGTATGATCTCTCGAGGACACACTGGCACCAACCA	300
Qy	301	ACGTTCCCTCCAGGAGCGGACACGCTGGCGCCCAACCCGGAGACTACGATGACCG	360
Db	301	ACGTTCCCTCCAGGAGCGGACACGCTGGCGCCCAACCCGGAGACTACGATGACCG	360
Qy	361	CCGTCAACCCCGAAGAGGAGGCGGATGGGACACAGCTGGACCCGAGGGAGCGTGA	420
Db	361	CCGTCAACCCCGAAGAGGAGGCGGATGGGACACAGCTGGACCCGAGGGAGCGTGA	420
Qy	421	AAGAGAAAGACTGGAGACAAACAGAGAAAGATTGGAGGCGACCAAGTCATCAGCAGCC	480
Db	421	AAGAGAAAGACTGGAGACAAACAGAGAAAGATTGGAGGCGACCAAGTCATCAGCAGCC	480
Qy	481	ACGAAATTAAGCCCGAAGAGAGAGAGAAACAGAGTGGGAAACACAGTAGCCA	540
Db	481	ACGAAATTAAGCCCGAAGAGAGAGAGAAACAGAGTGGGAAACACAGTAGCCA	540
Qy	541	TGTAGGGAAGAAACATCTCGGAACACCTTTCTACTCCCGTCAAGGCGGTTTAGCAC	600
Db	541	TGTAGGGAAGAAACATCTCGGAACACCTTTCTACTCCCGTCAAGGCGGTTTAGCAC	600
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Db	601	CCGCTACGGGAAACAAACCGTAGGATCCGGGCTCTGACAGAGTTTGAACAAAGTCAAG	660
Qy	661	GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720
Db	661	GCAGTTTCAGAACTCCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTAACACTCT	720
Qy	721	TGTTCTTCCCAAGCAGCTGATCTGATAACATCTTGTATCCAGCAAGGGCAAGCCAC	780
Db	721	TGTTCTTCCCAAGCAGCTGATCTGATAACATCTTGTATCCAGCAAGGGCAAGCCAC	780
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Db	781	CGTGACCGTAGCAATAGCAATTAACAGAAAGAGCTTTAATCTTTGACGAGGCCATGCAC	840
Qy	841	CAGAAATCCATCCGGTTTCATCTTACATCTTGAACCCGCATGACCAACAGAACTCAG	900
Db	841	CAGAAATCCATCCGGTTTCATCTTACATCTTGAACCCGCATGACCAACAGAACTCAG	900
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Db	901	AGTAGCTTAAATCTCCATGCCGTTTAAACACCCCGCCAGTTTGAGGATTTCTTCCCGG	960
Qy	961	GAGCAGCCGAGACCAATCTACTTTCAGGGGCTTCAGCAGGAATACGTTGGAGGCCG	1020
Db	961	GAGCAGCCGAGACCAATCTACTTTCAGGGGCTTCAGCAGGAATACGTTGGAGGCCG	1020
Qy	1021	CTTCAATGCGGAATTCATAGAGATACGAGGGTGTCTTTAGAGAGATGTCAGGAGTGA	1080
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RESULT 3
AR716329
LOCUS
DEFINITION
ACCESSION
VERSION

AR716329 2032 bp DNA linear PAT 07-OCT-2005
Sequence 5 from patent US 6943010.
AR716329.1 GI:77364704

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Db
1921 TTTTAACGTAGAAATGGAGGCAACTTGTATGTATCGATAATAAGATCACGCTTTGTACT 1980
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1981 CTACTATCCAAAACCTTATCAATAAATAAATAAAGCTTTGTGGTGTCTTCTCC 2032

RESULT 4
AX148742
LOCUS AX148742 2032 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 5 from Patent WO0136621.
ACCESSION AX148742
VERSION AX148742.1 GI:14347296
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1
REFERENCE
AUTHORS Dodo,H.W., Arntzen,C.J., Konan,K.N. and Viquez,O.M.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: WO 0136621-A 5 25-MAY-2001;
Alabama A & M University (US)
FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 2032; DB 2; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATAATCATATATATCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGGGAG 60
Db
1 AATAATCATATATATCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGGGAG 60
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Db
61 GGTTTCTCCACTGATGCTGTGTAGGGATCCTTGTCTGGCTTCAGTTTCTGCAACGCA 120
QY 121 TGCCAAGTATACCTTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
Db
121 TGCCAAGTATACCTTTACAGAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
QY 181 GAGTTGTCAACAGAACCGATGACTTGAAGCAAAAGGCGATGCGAGTCTGCTGCACCAA 240
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QY 421 AAGAGAAGAAGACTGAGAGACAAACAGAGAAGATTGGAGGCGCACCAAGTCAATCAGCAGCC 480
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QY 481 ACGGAAAAATAAGGCCCCGAGAGAGAGAGAGGAGAACAGAGTGGGGAACACACAGGTAGCCA 540

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Db	1621	CGAATCCATCTCTGGCTTCGGTATCAACGCTGAAACAAACACAGAAATCTTCTTGC	1680
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ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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1 (bases 1 to 2032)			
Burke,A.W., Cockrell,G., Stanley,J.S., Helm,R.M. and Bannon,G.A. Recombinant peanut allergen Ara h I expression and IgE binding in patients with peanut hypersensitivity J. Clin. Invest. 96 (4), 1715-1721 (1995)			
7560062			
On Dec 16, 1994 this sequence version replaced gi:508640.			
Original source text: Arachis hypogaea (strain Florunner).			
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5'-UTR			
CDS			

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Qy	121	TGCCAAGTCATCACCTTACAGAGAAAAACAGAGAAACCCCTCGCCACAGAGGTGCCTCCA	180
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Qy	181	GAGTTGTCAACAGGAACCGGATGACTTTGAAGCAAAAGGCGATCGGAGTCTCGCTGCACCAA	240
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Qy	241	GCTCGAGTATGATCCTCGTTGTCTATGATCTCTCGAGGACACACTGGCACCACCAACCA	300
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Qy	301	AGTTTCCCTCCAGGGGAGCGGACACGTCGCGCCGCAACCCGGAGACTACGATGATGACCG	360
Db	301	AGTTTCCCTCCAGGGGAGCGGACACGTCGCGCCGCAACCCGGAGACTACGATGATGACCG	360
Qy	361	CGTCAACCCCGAAGAGAGAGAGCGCGATGGGGACACGCTGGACCCGAGGGAGCGTGA	420
Db	361	CGTCAACCCCGAAGAGAGAGAGCGCGATGGGGACACGCTGGACCCGAGGGAGCGTGA	420
Qy	421	AAGAGAAAGAACTGGAGACAACCAAGAGAAGATTGGAGGCGGACCAAGTCATCAGCAGCC	480
Db	421	AAGAGAAAGAACTGGAGACAACCAAGAGAAGATTGGAGGCGGACCAAGTCATCAGCAGCC	480
Qy	481	ACGGAATAAAGGCCCGAAGAGAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	540
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Qy	721	TGTTCTTCCCAAGCAGCTGATCTGATTAACATCTCTTTATCCAGCAAGGGCAAGCCAC	780
Db	721	TGTTCTTCCCAAGCAGCTGATCTGATTAACATCTCTTTATCCAGCAAGGGCAAGCCAC	780
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Db	1921	TTTTAACTGAGAATGGAGCAACTTGTATTGTATCGATAATAAGATCACGCTTTTGTACT	1980
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LOCUS	AR257470	2041 bp	DNA linear PAT 20-DEC-2002
DEFINITION	Sequence 23 from patent US 6486311.		
ACCESSION	AR257470		
VERSION	AR257470.1	GI:27307483	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2041)		
AUTHORS	Burks, A.W. Jr., Stanley, J.S., Cockrell, G., King, N.E., Sampson, H.A., Helm, R.M. and Bannon, G.A.		
TITLE	Peanut allergens and methods		
JOURNAL	Patent: US 6486311-A 23 26-NOV-2002; Mt. Sinai School of Medicine and University of Arkansas; New York, NY		
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Qy	121	TGCCAGTGCATCCTTACCAGAGAAACAGAGAACCCCTGCGCCACAGAGGTGCCTCCA	180
Db	121	TGCCAGTGCATCCTTACCAGAGAAACAGAGAACCCCTGCGCCACAGAGGTGCCTCCA	180
Qy	181	GAGTTGTCAACAGGAACCGGATGACCTTGAAGCAAAAAGGCATGCGAGTCTCGCTGCACCAA	240
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Qy	241	GCTCGAGTATGATCCTCGTTGTCTGTATGATCCTCGAGGACACACTGGCAACCAACCA	300
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Qy	301	ACGTTCCCTCCAGGGGAGCGGACACGTGGCCGCCCAACCCGGAGATCTACGATGATGACCG	360
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Qy	481	ACGGAATAAAGCCCGAAGGAAGAGAGAGAAACAAAGTGGGGAAACACACAGGTAGCCA	540
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QY	661	GCAGTTTCAGAAATCTCAGAAATCACCGTATTTGTCAGATCGAGGCCAAACCTTAACACTCT	720
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QY	901	AGTAGCTAAATCTCCATGCCCTTAAACACCGGCCAGTTTGAGGATTTCTTCCGGC	960
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DEFINITION	Sequence 4 from Patent WO0140264.		
ACCESSION	AX155331		
VERSION	AX155331.1	GI:14536766	
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ORGANISM	Arachis hypogaea		
REFERENCE	Bannon, G.A., Burks, W.A., Caplan, M.J., Sampson, H. and Sosin, H.		
AUTHORS	Peptide antigens		
TITLE	Patent: WO 0140264-A 4 07-JUN-2001;		
JOURNAL	Panacea Pharmaceuticals, LLC (US); The University of Arkansas (US)		
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Methods and reagents for decreasing allergic reactions.
BD107898
BD107898.1 GI:23202716
JP 2002501748-A/1.
unidentified
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Methods and reagents for decreasing allergic reactions
Patent: JP 2002501748-A 1 22-JAN-2002;
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UNIVERSITY OF NEW YORK, HOWARD SOSIN
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PD 22-JAN-2002
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13-FEB-1998 US 60/074624,13-FEB-1998 US 60/074633 PR

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REFERENCE Bannon, G.A.; Burks, W.A.; Caplan, M.J.; Sampson, H. and Sosin, H.
AUTHORS Peptide antigens
TITLE Patent: WO 0140264-A 5 07-JUN-2001;
JOURNAL Panacea Pharmaceuticals, LLC (US); The University of Arkansas (US);
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Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and
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Qy 1248 TGAGAGAGCGGAGCCCGATCTTTCTAAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307
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RESULT 14

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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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1. 2
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Original source text: Arachis hypogaea (strain Florunner) Seed cDNA
to mRNA.
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Arachis hypogaea (clone P17) Ara h I mRNA, complete cds.
L38853.1 GI:620024
peanut hypersensitivity.
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 1949)
Burke,A.W., Cockrell,G., Stanley,J.S., Helm,R.M. and Bannon,G.A.
Recombinant peanut allergen Ara h I expression and IgE binding in
patients with peanut hypersensitivity
Unpublished (1994)
Original source text: Arachis hypogaea (strain Florunner) Seed cDNA
to mRNA.
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3'UTR

polyA_site

ORIGIN

Query Match 85.2%; Score 1752.4; DB 4; Length 1949;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;

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Search completed: June 23, 2006, 18:12:39
Job time : 11863.6 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2006, 09:14:45 ; Search time 905.436 Seconds

(without alignments)
15647.278 Million cell updates/sec

Title: US-10-728-051-1

Perfect score: 2032

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
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 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
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 - 13: Geneseqn2004bs:*
 - 14: Geneseqn2005s:*
 - 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2032	100.0	2032	4	Aaf90339 Peanut al
2	2032	100.0	2032	8	Abx70603 Peanut Ar
3	2032	100.0	2032	10	Adg27462 Peanut Ar
4	2032	100.0	2032	14	Adv97537 Peanut Ar
5	2032	100.0	2040	14	Adv97600 Peanut Ar
6	2032	100.0	2041	4	Aas08537 DNA encod
7	2025.6	99.7	2032	2	Aat76613 Peanut al
8	1930	95.0	1930	2	Aaz06382 Peanut al
9	1752.4	86.2	1949	2	Aat76612 Peanut al
10	1752.4	86.2	1949	8	Abx70604 Peanut Ar
11	1752.4	86.2	1949	14	Adv97536 Peanut Ar
12	1750.8	86.2	1949	10	Adg27463 Peanut Ar
13	1749.8	86.1	1952	4	Aas08539 Anaphylac
14	1324	65.2	1340	14	Adv97605 Peanut Ar
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16	406.8	20.0	1254	9	Acc49562 Mature be
17	406.8	20.0	1278	9	Acc49561 FLAG-taggr
18	406.8	20.0	1320	2	Aav17564 Coding se

19	406.8	20.0	1320	9	ACC49553	Acc49553 Glycine m
20	404	19.9	1632	6	ABs55198	ABs55198 Glycine m
21	404	19.9	1818	2	Aav17562	Aav17562 Coding se
22	404	19.9	2073	13	ADT17970	ADT17970 Plant cdn
23	402	19.8	1680	6	ABs55197	ABs55197 Glycine m
24	390	19.2	1656	13	ADx14996	ADx14996 Plant ful
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26	293.4	14.4	1107	13	ADx13542	ADx13542 Plant ful
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38	199.6	9.8	720	13	ADx32347	ADx32347 Plant ful
39	186	9.2	673	13	ADx13078	ADx13078 Plant ful
40	167.2	8.2	641	13	ADx13996	ADx13996 Plant ful
41	160.2	7.9	2140	2	AAV42316	AAV42316 Macadamia
42	158.2	7.8	614	13	ADx13556	ADx13556 Plant ful
43	157.4	7.7	2171	2	AAV42311	AAV42311 Macadamia
44	152.6	7.5	2171	2	AAV42310	AAV42310 Macadamia
45	141.8	7.0	536	13	ADx13016	ADx13016 Plant ful

ALIGNMENTS

RESULT 1

AAF90339

ID AAF90339 standard; cdna; 2032 BP.

XX AAF90339;

XX 11-SEP-2003 (revised)

DT 23-JUL-2001 (first entry)

XX Peanut allergen Ara hl P41B cdna.

DE Peanut allergen Ara hl P41B cdna.

XX Peanut; allergen; Ara hl P41B; transgenic plant; allergy; ss.

XX Arachis hypogaea.

OS

XX Key misc_feature

FT Location/Qualifiers

FT 676..930

FT /*tag= a

FT /note= "PCR amplified fragment"

XX WO200136621-A2.

XX 25-MAY-2001.

XX 20-NOV-2000; 2000WO-US031657.

XX 19-NOV-1999; 99US-0167255P.

XX (UYAL-) UNIV ALABAMA A & M.

PA Dodo HW, Arntzen CJ, Konan KN, Viquez OM;

XX WPI; 2001-355630/37.

XX Producing transgenic peanut plants that produce allergen-free seeds,

PT useful in non-allergenic foods, by antisense or sense co-suppression of

PT allergen-encoding genes.

XX Claim 20; Fig 5; 72pp; English.

PS The present sequence is that of peanut allergen Ara hl P41B cdna. A

XX

CC

CC portion of this gene is homologous to the corresponding region of the
CC peanut allergen Ara hi P17 gene. This region has been PCR amplified,
CC cloned in transformation vectors (pUC18 and pBl4434) in sense and
CC antisense orientations and used to down-regulate Ara hi P41B and Ara hi
CC P17 allergens in peanut. This is an example of the method of the
CC invention, which relates to the production of a peanut plant having
CC reduced, or undetectable, allergenic protein (AP) content in its seed. A
CC peanut plant cell is transformed with a DNA construct containing an
CC antisense AP gene and/or sense AP gene, or their fragments, regenerated
CC to plants, and fertile transgenic plants that produce seeds with reduced
CC AP content are identified. The seeds are useful for preparation of
CC allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 2032 BP; 628 A; 473 C; 530 G; 401 T; 0 U; 0 Other;

Query Match 100.0%; Score 2032; DB 4; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGGAG 60
DB 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGGAG 60
QY 61 GGTTCCTCCACTGATGCTGTGTAGGGATCCTGTCTGGCTTCAGTTTCTGCAACGCA 120
DB 61 GGTTCCTCCACTGATGCTGTGTAGGGATCCTGTCTGGCTTCAGTTTCTGCAACGCA 120
QY 121 TGCCAAAGTCATACCTTTACAGAGAAACACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
DB 121 TGCCAAAGTCATACCTTTACAGAGAAACACAGAGAACCCCTGCGCCAGAGGTGCCTCCA 180
QY 181 GAGTTGTCAACAGAACCCGATGACTTTGAAGCAAAAGGCATGCGAGTCTCGCTGCAACCA 240
DB 181 GAGTTGTCAACAGGAAACCCGATGACTTTGAAGCAAAAGGCATGCGAGTCTCGCTGCAACCA 240
QY 241 GCTCGAGTATGATCTCTGTTGCTGTATGATCTCTCGAGGACACACTGGCACCAACCAACCA 300
DB 241 GCTCGAGTATGATCTCTGTTGCTGTATGATCTCTCGAGGACACACTGGGCACCAACCA 300
QY 301 ACCTTCCCCTCCAGGGGACGGACACGTCGCCGCCCAACCCGGAGACTACGATGATGACCG 360
DB 301 ACCTTCCCCTCCAGGGGACGGACACGTCGCCGCCCAACCCGGAGACTACGATGATGACCG 360
QY 361 CCCTCAACCCCGAAGAGAGAGAGGCGCGATGGGACCCAGCTGGACCGAGGAGCGTGA 420
DB 361 CCCTCAACCCCGAAGAGAGAGAGGCGCGATGGGACCCAGCTGGACCCGAGGAGCGTGA 420
QY 421 AAGAGAGAAGAGACTGGAGACAACCAAGAGAAGATTGGAGCGCACCAAGTCAATCAGCAGGCC 480
DB 421 AAGAGAGAAGAGACTGGAGACAACCAAGAGAAGATTGGAGCGCACCAAGTCAATCAGCAGGCC 480
QY 481 ACGGAAAAATAAGCCCGAAGGAAGAGAGAGAAACAAGAGTGGGGAAACACACAGGTAGCCA 540
DB 481 ACGGAAAAATAAGCCCGAAGGAAGAGAGAGAAACAAGAGTGGGGAAACACACAGGTAGCCA 540
QY 541 TGTGAGGGAAGAACATCTCGGAACACCCCTTTCTACTTCCCTCAAGGCGGTTTAGCAC 600
DB 541 TGTGAGGGAAGAACATCTCGGAACACCCCTTTCTACTTCCCTCAAGGCGGTTTAGCAC 600
QY 601 CCCTACGGGAACCAAAACCGGTAGGATCCGGGTCTCGAGAGGTTTGAACCAAGGTCAAG 660
DB 601 CCCTACGGGAACCAAAACCGGTAGGATCCGGGTCTCGAGAGGTTTGAACCAAGGTCAAG 660
QY 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTGCGAGATCGAGGCCAAACCTAACACTCT 720
DB 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTGCGAGATCGAGGCCAAACCTAACACTCT 720
QY 721 TGTTCCTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGCAAGGGCAAGCCAC 780
DB 721 TGTTCCTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGCAAGGGCAAGCCAC 780
QY 781 CGTGACCGTAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTTGACGAGGGCCATGCAC 840
DB 781 CGTGACCGTAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTTTCAATTTTGAAGGC 1920

DB 781 CGTGACCGTAGCAATGGCAATTAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCAC 840
QY 841 CAGAAATCCCATCCGGTTTCATTTCTTACATCTTTGAAACCGCCATGACAAACAGAACTCAG 900
DB 841 CAGAAATCCCATCCGGTTTCATTTCTTACATCTTTGAAACCGCCATGACAAACAGAACTCAG 900
QY 901 AGTAGTAAATCTCCATCCGCTTAAACACACCCCGCCAGTTTGAGGATTTCTTCCCGGC 960
DB 901 AGTAGTAAATCTCCATCCGCTTAAACACACCCCGCCAGTTTGAGGATTTCTTCCCGGC 960
QY 961 GAGCAGCCGAGACCAATCATCTTCTGAGGGCTTCAGCAGGAATACGTTGGAGCCGC 1020
DB 961 GAGCAGCCGAGACCAATCATCTTCTGAGGGCTTCAGCAGGAATACGTTGGAGCCGC 1020
QY 1021 CTTCAATGCGGAATTCATAGATACGAGGGTGTCTGTTAGAGAAATTCAGGAGGTGA 1080
DB 1021 CTTCAATGCGGAATTCATAGATACGAGGGTGTCTGTTAGAGAAATTCAGGAGGTGA 1080
QY 1081 GCAAGAGGAGAGGGCAGAGGCGATGGAGTACTCGAGTAGTGAGAAACAATGAAGGAGT 1140
DB 1081 GCAAGAGGAGAGGGCAGAGGCGATGGAGTACTCGAGTAGTGAGAAACAATGAAGGAGT 1140
QY 1141 GATAGTCAAAGTGTCAAAGGAGCAGTTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTC 1200
DB 1141 GATAGTCAAAGTGTCAAAGGAGCAGCGTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTC 1200
QY 1201 AAAGAAAGCTCCGAAGAGAGGGAGATATCACCACCCCAATCACTTGAGAGAGGCGA 1260
DB 1201 AAAGAAAGCTCCGAAGAGAGGGAGATATCACCACCCCAATCACTTGAGAGAGGCGA 1260
QY 1261 GCCCGATCTTTCTAAACAATTTGGGAAGTTATTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
DB 1261 GCCCGATCTTTCTAAACAATTTGGGAAGTTATTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
QY 1321 CCAGCTTCAGGACCTGGACATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
DB 1321 CCAGCTTCAGGACCTGGACATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
QY 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCGTCGTCACAAAGGAACTGGAA 1440
DB 1381 GCTCCACACTTCAACTCAAGGCCATGGTTATCGTCGTCGTCACAAAGGAACTGGAA 1440
QY 1441 CTTTGAATCTGTGGCTGTAAAGAAAGAGCAACAAGAGGGGACGGGGAAGAGGA 1500
DB 1441 CTTTGAATCTGTGGCTGTAAAGAAAGAGCAACAAGAGGGGACGGGGAAGAGGA 1500
QY 1501 GGAACGAAGACGAAGAGAGAGGAAAGTAAACAGAGAGGTGCGTAGGTACAACAGCGAGTT 1560
DB 1501 GGAACGAAGACGAAGAGAGAGGAAAGTAAACAGAGAGGTGCGTAGGTACAACAGCGAGTT 1560
QY 1561 GAAGGAGGCGATGTCTCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC 1620
DB 1561 GAAGGAGGCGATGTCTCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCCTC 1620
QY 1621 CGAATCTCAATCTGCTTGGCTTCGGTATCAACGCTGAAAAACAACACAGAAATCTTCTTGC 1680
DB 1621 CGAATCTCAATCTGCTTGGCTTCGGTATCAACGCTGAAAAACAACACAGAAATCTTCTTGC 1680
QY 1681 AGGTGATAAGGACAATGTGATAGACAGATAGAGAGAGGAGGAGGATTTAGCATTTCC 1740
DB 1681 AGGTGATAAGGACAATGTGATAGACAGATAGAGAGAGGAGGAGGATTTAGCATTTCC 1740
QY 1741 TGGGTCCGGTGAACAAGTTGAGAAGCTCATCAAAAACAGAGGAATCTCAGTTTGTAG 1800
DB 1741 TGGGTCCGGTGAACAAGTTGAGAAGCTCATCAAAAACAGAGGAATCTCAGTTTGTAG 1800
QY 1801 TGTCTGCTCAATCTCAATCTCAATCTCCGCTGCTCTCTGAGAAAAAGAGTCTCCTGAGAA 1860
DB 1801 TGTCTGCTCAATCTCAATCTCAATCTCCGCTGCTCTCTGAGAAAAAGAGTCTCCTGAGAA 1860
QY 1861 AGAGGATCAAGAGGAGGAGAAAAACCAAGAGGGGAGGAGGTCACCTCTTCAATTTTGAAGGC 1920
DB 1861 AGAGGATCAAGAGGAGGAGAAAAACCAAGAGGGGAGGAGGTCACCTCTTCAATTTTGAAGGC 1920

Db 1081 ||||| GCAGAGGAGAGAGGAGAGGATGAGTATCGGAGTAGTGAGAAATGAAGAGT 1140
Qy 1141 GATAGTCAAAAGTGTCAAAGAGAGACGTTGAAGAACTTACTTAAGACACGCTAAATCCGTCTC 1200
Db 1141 GATAGTCAAAAGTGTCAAAGAGAGACGTTGAAGAACTTACTTAAGACACGCTAAATCCGTCTC 1200
Qy 1201 AAGAAGGCTCCGAAGAAGAGAGAGATATCAACAACCCCAATCACTTGAGAGAAGCGGA 1260
Db 1201 AAGAAGGCTCCGAAGAAGAGAGAGATATCAACAACCCCAATCACTTGAGAGAAGCGGA 1260
Qy 1261 GCCGATCTTTCTAACAACCTTTGGGAGTTATTTGAGGTGAAGCCAGACAAGAGAACC 1320
Db 1261 GCCGATCTTTCTAACAACCTTTGGGAGTTATTTGAGGTGAAGCCAGACAAGAGAACC 1320
Qy 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGAT 1380
Db 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAGAAGGAGCTTTGAT 1380
Qy 1381 GTCCTCACACTTCAACTCAAAAGGCCATGGTTATCGTCGTCAACAAGGAACTCGAAA 1440
Db 1381 GTCCTCACACTTCAACTCAAAAGGCCATGGTTATCGTCGTCAACAAGGAACTCGAAA 1440
Qy 1441 CTTGAACTCGTGGCTGTAGAAAGAGCAACAACAGAGGGGACGCGGGAAGAAGGA 1500
Db 1441 CTTGAACTCGTGGCTGTAGAAAGAGCAACAACAGAGGGGACGCGGGAAGAAGGA 1500
Qy 1501 GGACGAAGACGAAGAAGAGAGAGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560
Db 1501 GGACGAAGACGAAGAAGAGAGAGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560
Qy 1561 GAAGGAAGGCGATGTTTCATCATATGCCAGAGCTCATCCAGTAGCATCAACGCTTCTC 1620
Db 1561 GAAGGAAGGCGATGTTTCATCATATGCCAGAGCTCATCCAGTAGCATCAACGCTTCTC 1620
Qy 1621 CGAACTCCATCTCGTGGCTTCGGTATCAACGCTGAAACCAACAGCAATCTTCTTGC 1680
Db 1621 CGAACTCCATCTCGTGGCTTCGGTATCAACGCTGAAACCAACAGCAATCTTCTTGC 1680
Qy 1681 AGGTGATAAGGACAATGTGTATAGACACAGATAGAGAAGCAAGCAAGGATTTAGCATCCC 1740
Db 1681 AGGTGATAAGGACAATGTGTATAGACACAGATAGAGAAGCAAGCAAGGATTTAGCATCCC 1740
Qy 1741 TGGGTGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGCAAGCAATCTTCTTGTAG 1800
Db 1741 TGGGTGGGTGAACAAGTTGAGAAGCTCATCAAAAACCAAGCAAGCAATCTTCTTGTAG 1800
Qy 1801 TGCTCGTCCCTCAATCTCAATCTCAATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1860
Db 1801 TGCTCGTCCCTCAATCTCAATCTCAATCTCCGTCGTCTCCTGAGAAAGAGTCTCCTGAGAA 1860
Qy 1861 AGAGGATCAAGAGAGAGAAACCAAGAGGAGGAGGTCCTCTTCAATTTTGAAGC 1920
Db 1861 AGAGGATCAAGAGAGAGAAACCAAGAGGAGGAGGTCCTCTTCAATTTTGAAGC 1920
Qy 1921 TTTTAAGTGAAGTGAAGGCACTTGTATGATCGATATAGATCAAGCTTTTCTACT 1980
Db 1921 TTTTAAGTGAAGTGAAGGCACTTGTATGATCGATATAGATCAAGCTTTTCTACT 1980
Qy 1981 CTACTATCAAAAACCTTATCAATAAATAAAGGTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCAAAAACCTTATCAATAAATAAAGGTTGTGCGTTGTTCTCC 2032

RESULT 3
ADG27462
ID ADG27462 standard; cDNA; 2032 BP.

XX AC ADG27462;

XX DT 26-FEB-2004 (first entry)

XX DE Peanut Ara h1 cDNA clone P41b.

XX KW Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3;
KW glycinin A2B1a; Jug n1; antiallergic; vulnery;
KW anaphylactic food allergen; IgE; allergy; wound.
XX OS Arachis hypogaea.
XX PN US2003202980-A1.
XX PD 30-OCT-2003.
XX XX 18-MAR-2002; 2002US-00100303.
XX PF 29-DEC-1995; 95US-0009455P.
XX PR 23-SEP-1996; 96US-00717933.
XX PR 31-JAN-1998; 98US-0073283P.
XX PR 13-FEB-1998; 98US-0074590P.
XX PR 13-FEB-1998; 98US-0074624P.
XX PR 13-FEB-1998; 98US-0074633P.
XX PR 29-JUN-1998; 98US-00106872.
XX PR 27-AUG-1998; 98US-00141220.
XX PR 13-NOV-1998; 98US-00191593.
XX PR 29-JAN-1999; 99US-00240557.
XX PR 29-JAN-1999; 99US-00241101.
XX PR 11-FEB-1999; 99US-00248673.
XX PR 11-FEB-1999; 99US-00248674.
XX PR 02-MAR-1999; 99US-0122450P.
XX PR 02-MAR-1999; 99US-0122452P.
XX PR 02-MAR-1999; 99US-0122560P.
XX PR 02-MAR-1999; 99US-0122565P.
XX PR 02-MAR-1999; 99US-0122566P.
XX PR 11-MAR-1999; 99US-00267719.
XX PR 28-JAN-2000; 2000US-00494096.
XX PR 16-MAR-2001; 2001US-0276822P.
XX (CAPL/) CAPLAN M J.
PA (SOSI/) SOSIN H B.
PA (SAMP/) SAMPSON H.
PA (BANN/) BANNON G A.
PA (BURK/) BURKS A W.
PA (COCK/) COCKRELL G.
PA (COMP/) COMPADRE C M.
PA (CONN/) CONNAUGHTON C.
PA (HELM/) HELM R M.
PA (KING/) KING N E.
PA (KOPP/) KOPPER R A.
PA (MALE/) MALEKI S J.
PA (RABJ/) RABJOHN P A.
PA (SHIN/) SHIN D S.
PA (STAN/) STANLEY J S.
XX Caplan MJ, Sosin HB, Sampson H, Bannan GA, Burks AW, Cockrell G;
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
PI Rabinjohn PA, Shin DS, Stanley JS;
XX WPI: 2003-875632/81.
DR P-PSDB; ADG27464.
XX PT New modified anaphylactic food allergen comprising a cysteine residue
PT which has been modified so that it cannot participate in the disulfide
PT bond, useful for treating allergic reactions or wounds.
XX PS Example 4; SEQ ID NO 5; 194pp; English.
XX CC The invention relates to a modified anaphylactic food allergen whose
CC amino acid sequence is substantially identical to that of a natural
CC anaphylactic food allergen. The natural anaphylactic food allergen
CC includes at least one cysteine residue that participates in a disulphide
CC bond when the natural anaphylactic food allergen is in its native
CC conformation, except that the cysteine residue has been modified so that
CC it cannot participate in the disulphide bond. Also included are a method
CC of making a modified anaphylactic food allergen, a nucleotide molecule
CC encoding a modified anaphylactic food allergen defined above, a

Db 961 GAGCAGCGAGACCAATCATCTCTTTCGAGGGCTTCAGCAGGAATACGTTGGAGCGC 1020
Qy 1021 CTTCAATGCGGAATTCATAGATACGAGGCTGCTGTAGAGAGAAATCAGGAGGTGA 1080
Db 1021 CTTCAATGCGGAATTCATAGATACGAGGCTGCTGTAGAGAGAAATCAGGAGGTGA 1080
Qy 1081 GCAAGAGGAGAGGGCAGAGCGGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140
Db 1081 GCAAGAGGAGAGGGCAGAGCGGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140
Qy 1141 GATAGTCAAGAGTCAAGAGAGCAGTGTGAAGAACTTACTAAGCAGCGTAAATCCGTC 1200
Db 1141 GATAGTCAAGAGTGTCAAGAGAGCAGTGTGAAGAACTTACTAAGCAGCGTAAATCCGTC 1200
Qy 1201 AAGAAAGAGCTCCGAAGAGAGGAGATATACCAACCCCAATCAACTTTGAGAGAGCGGA 1260
Db 1201 AAGAAAGAGCTCCGAAGAGAGGAGATATACCAACCCCAATCAACTTTGAGAGAGCGGA 1260
Qy 1261 GCCGATCTTTTCTAACAACTTTGGGAAAGTTATTGAGGTGAAGCCAGAACGAACCC 1320
Db 1261 GCCGATCTTTTCTAACAACTTTGGGAAAGTTATTGAGGTGAAGCCAGAACGAACCC 1320
Qy 1321 CCAGCTTCAGGACTGACATGATGCTCAGCTGTGTAGAGATCAAGAGAGGCTTTGAT 1380
Db 1321 CCAGCTTCAGGACTGACATGATGCTCAGCTGTGTAGAGATCAAGAGAGGCTTTGAT 1380
Qy 1381 GCTCCACACCTTCAACTCAAGGCCATGTTATCGTCGTCAACAAAGGAACTCGGAA 1440
Db 1381 GCTCCACACCTTCAACTCAAGGCCATGTTATCGTCGTCAACAAAGGAACTCGGAA 1440
Qy 1441 CTTGAACTCGTGGCTTAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGA 1500
Db 1441 CTTGAACTCGTGGCTTAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAAGGA 1500
Qy 1501 GGAAGAGAGCAAGAGAGAGGAGGAGTAACAGAGAGGTCGTAGGTACACAGCGAGTT 1560
Db 1501 GGAAGAGAGCAAGAGAGAGGAGGAGTAACAGAGAGGTCGTAGGTACACAGCGAGTT 1560
Qy 1561 GAAGGAGGCGATGTTTCATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGCTTCC 1620
Db 1561 GAAGGAGGCGATGTTTCATCATGCGCAGCAGCTCATCCAGTAGCCATCAACGCTTCC 1620
Qy 1621 CGAATCCATCTGCTGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTGC 1680
Db 1621 CGAATCCATCTGCTGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTGC 1680
Qy 1681 AGGTGATAAGGACAAATGTGTAGACACAGATAGAGAACAGGAAAGGATTTAGCATCC 1740
Db 1681 AGGTGATAAGGACAAATGTGTAGACACAGATAGAGAACAGGAAAGGATTTAGCATCC 1740
Qy 1741 TGGGTCGGGTGAACAGTTGAGAGCTCATCAAAACCAAGAAATCTCACTTTGTAG 1800
Db 1741 TGGGTCGGGTGAACAGTTGAGAGCTCATCAAAACCAAGAAATCTCACTTTGTAG 1800
Qy 1801 TGCTCGCTCAATCTCAATCTCAATCTCGTCTGCTGAGAGAGGTCCTCAGAA 1860
Db 1801 TGCTCGCTCAATCTCAATCTCAATCTCGTCTGCTGAGAGAGGTCCTCAGAA 1860
Qy 1861 AGAGGATCAAGAGAGGAGAAACCAAGAGGAGGAGGTCCTCTTCAATTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGAGGAGAAACCAAGAGGAGGAGGTCCTCTTCAATTTGAAGGC 1920
Qy 1921 TTTTAACTGAGATGGAGCACTTGTATGATCGATATAGATCAAGCTTTTGTACT 1980
Db 1921 TTTTAACTGAGATGGAGCACTTGTATGATCGATATAGATCAAGCTTTTGTACT 1980
Qy 1981 CTACTATCCAAAAAATCTATCAATAAATAAAGGTTGTGCGTGTGTTCTCC 2032
Db 1981 CTACTATCCAAAAAATCTATCAATAAATAAAGGTTGTGCGTGTGTTCTCC 2032

ADV97600
ID ADV97600 standard; cDNA; 2040 BP.
XX AC ADV97600;
XX DT 10-MAR-2005 (first entry)
XX Peanut Ara h I allergen alpha P17 cDNA encoding a seed storage protein.
DE allergen; atopic dermatitis; diagnostic; immunotherapy;
KW immediate type hypersensitivity; Ara h I; dermatological; antiallergic;
KW immunosuppressive; antibody engineering; gene; ss.
XX Arachis hypogaea.
XX Location/Qualifiers
PH Key 50..1930
FT CDS /tag= a
FT /product= "Ara h I allergen protein (P17 clone)"
XX US6835824-B1.
XX 28-DEC-2004.
XX 13-NOV-1998; 98US-00191593.
XX 29-DEC-1995; 95US-0009455P.
XX 23-SEP-1996; 96US-0071933.
XX (UYAR-) UNIV ARKANSAS.
XX Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX WPI; 2005-045982/05.
XX P-PSDB; ADV97601.
XX New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
XX obtaining diagnostics with optimal concentrations of each allergen, for
XX developing panels of mixtures of recombinant allergens, and in
XX immunotherapy.
XX Disclosure; Fig 16; 14pp; English.
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX the peanut allergen Ara h I that has been identified in patients with
XX atopic dermatitis. Specifically, it refers to a monoclonal antibody
XX enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the
XX peanut allergens, where the monoclonal antibodies have specificity for a
XX selected peanut allergen antigen. The present invention also describes
XX hybridomas that produce two-site monoclonal antibodies specific for a
XX peanut allergen that can be used in an ELISA to detect and determine the
XX concentration of a specific peanut allergen in a food product or in food
XX processing. Furthermore, it provides an expression vector and the
XX isolated nucleic acid or its fraction can include a diagnostic label.
XX Accordingly, these nucleic acids are useful for obtaining diagnostics
XX with optimal concentrations of each allergen or for developing panels of
XX mixtures of large numbers of recombinant allergens such that it can be
XX used in immunotherapy for the treatment of food hypersensitivity
XX reactions. This polynucleotide sequence is the peanut Ara h I allergen
XX cDNA (P17 clone) of the invention.
XX Sequence 2040 BP; 636 A; 473 C; 530 G; 401 T; 0 U; 0 Other;
Query Match 100.0%; Score 2032; DB 14; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGGGAG 60
Db 1 AATAATCATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGGGAG 60
Qy 61 GGTTCCTCCACTGATGCTGTGCTAGGATCCTGTGCTGGCTTCACTTCTGCAACGCA 120

Db 61 GGTTCCTCCTACTGATGCTGTTGCTAGGGATCCTTGTCTCCTGGCTTCAGTTTCTCGAAGCA 120
Qy 121 TGCCAAGTTCATCACTTTACAGAGAAACACAGAGAAACCCCTGCGCCACAGAGTGCTCTCCA 180
Db 121 TGCCAAGTTCATCACTTTACAGAGAAACACAGAGAAACCCCTGCGCCACAGAGTGCTCTCCA 180
Qy 181 GAGTTGTCAACAGAACCGGATGACTTGAAGCAAAAGGCGATGCGAGTCTCGTGCACCAA 240
Db 181 GAGTTGTCAACAGGAAACCGGATGACTTGAAGCAAAAGGCGATGCGAGTCTCGTGCACCAA 240
Qy 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACATGGGACACCAACCA 300
Db 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACATGGGACACCAACCA 300
Qy 301 ACCTTCCCCTCCAGGGGACGGACACGCTGGCCGCCAAACCCGGAGACTACGATGATGCCG 360
Db 301 ACCTTCCCCTCCAGGGGACGGACACGCTGGCCGCCAAACCCGGAGACTACGATGATGCCG 360
Qy 361 CCCTCAACCCCGAAG 420
Db 361 CCCTCAACCCCGAAG 420
Qy 421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGCGGACCAAGTCAATCAGCAGCC 480
Db 421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGCGGACCAAGTCAATCAGCAGCC 480
Qy 481 ACGGAAATAAGGCCCGGAAAG 540
Db 481 ACGGAAATAAGGCCCGGAAAG 540
Qy 541 TGTGAGGAGAAACATCTCTCGGAACACCCCTTTCTACTTCCCTCAAGGGCGTTTAGCAC 600
Db 541 TGTGAGGAGAAACATCTCTCGGAACACCCCTTTCTACTTCCCTCAAGGGCGTTTAGCAC 600
Qy 601 CCCTACGGGAACCAAAACGGTAGGATCGGGTCTCTGCAGAGGTTTGACCAAGGTCAAG 660
Db 601 CCCTACGGGAACCAAAACGGTAGGATCGGGTCTCTGCAGAGGTTTGACCAAGAGTCAAG 660
Qy 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTGCAGATCGAGGCCAAACCTAACACTCT 720
Db 661 GCAGTTTCAGAAATCTCCAGAAATCACCGTATTTGTGCAGATCGAGGCCAAACCTAACACTCT 720
Qy 721 TGTCTCTCCAGCAGCTGATCTGATACATCTTGTATCCAGCAGAGGCGCAAGCCAC 780
Db 721 TGTCTCTCCAGCAGCTGATCTGATACATCTTGTATCCAGCAGAGGCGCAAGCCAC 780
Qy 781 CGTGACCGTAGCAATGGCAATAACAGAAAGAGCTTTAATCTTTGACGAGGGCCATGCACCT 840
Db 781 CGTGACCGTAGCAATGGCAATAACAGAAAGAGCTTTAATCTTTGACGAGGGCCATGCACCT 840
Qy 841 CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTTGAACCGCCATGACCAACAGAACTCAG 900
Db 841 CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTTGAACCGCCATGACCAACAGAACTCAG 900
Qy 901 AGTAGCTAAATCTCCATCCCGTTTACACACCCGGCCAGTTTCAGGATTTCTTCCCGGC 960
Db 901 AGTAGCTAAATCTCCATCCCGTTTACACACCCGGCCAGTTTCAGGATTTCTTCCCGGC 960
Qy 961 GAGCAGCCGAGACCAATCTCTACTTTGACGGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020
Db 961 GAGCAGCCGAGACCAATCTCTACTTTGACGGGCTTCAGCAGGAATACGTTGGAGGCCGC 1020
Qy 1021 CTTCAATGCGGAATTCATGAGATACGAGGGTGTCTTTAGAGAGAGATGACAGAGGTGA 1080
Db 1021 CTTCAATGCGGAATTCATGAGATACGAGGGTGTCTTTAGAGAGAGATGACAGAGGTGA 1080
Qy 1081 GCAGAGGAGAGGGCAGAGGGCGATGGAGTCTCGAGTAGTGAGAACTGAAGAGT 1140
Db 1081 GCAGAGGAGAGGGCAGAGGGCGATGGAGTCTCGAGTAGTGAGAACTGAAGAGT 1140
Qy 1141 GATAGTCAAAAGTGTCAAAAGGAGCAGGTTGAAGACTTTACTTAAGCAGCCTAAATCCGCTTC 1200
Db 1141 GATAGTCAAAAGTGTCAAAAGGAGCAGGTTGAAGACTTTACTTAAGCAGCCTAAATCCGCTTC 1200

Qy 1201 AAAGAAAGGCTCCGAAGAGAGAGAGATATACCAACCCAACTCAACTTGTAGAGAAAGCGGA 1260
Db 1201 AAAGAAAGGCTCCGAAGAGAGAGAGATATACCAACCCAACTCAACTTGTAGAGAAAGCGGA 1260
Qy 1261 GCCCGATCTTTCTAACAACCTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
Db 1261 GCCCGATCTTTCTAACAACCTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
Qy 1321 CCAGCTTCAGGACCTCGACATGATGCTCACTGTGTAGAGATCAAAAGAGGAGCTTTGTAT 1380
Db 1321 CCAGCTTCAGGACCTCGACATGATGCTCACTGTGTAGAGATCAAAAGAGGAGCTTTGTAT 1380
Qy 1381 GCTCCACACACTTCAACTCAAGGCCATGTTATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1440
Db 1381 GCTCCACACACTTCAACTCAAGGCCATGTTATCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1440
Qy 1441 CCTTGAACCTCGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAGGA 1500
Db 1441 CCTTGAACCTCGTGGCTGTAAAGAAAAGAGCAACACAGAGGGGACGGCGGAAGAGGA 1500
Qy 1501 GGACGGAAGACGAAGAGAGAGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560
Db 1501 GGACGGAAGACGAAGAGAGAGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTT 1560
Qy 1561 GAAGGAAGGGGATGCTGTTTCATCATGCCAGCAGCTCATCCAGTAGCCCATCAACGCTTCCTC 1620
Db 1561 GAAGGAAGGGGATGCTGTTTCATCATGCCAGCAGCTCATCCAGTAGCCCATCAACGCTTCCTC 1620
Qy 1621 CGAACTCCCATCTGCTTTGGCTTCGGTATCAACGCTGAAAACCAACACAGAGATCTTCTCTGC 1680
Db 1621 CGAACTCCCATCTGCTTTGGCTTCGGTATCAACGCTGAAAACCAACACAGAGATCTTCTCTGC 1680
Qy 1681 AGGTGATAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATTTCCC 1740
Db 1681 AGGTGATAAGGACAATGTGATAGACAGATAGAGAAAGCAAGCAAGGATTTAGCATTTCCC 1740
Qy 1741 TGGGTGGGTGAACAAGTTGAGNAAGCTCATCAAAACCCAGAGGAATCTCAGTTTGTGAG 1800
Db 1741 TGGGTGGGTGAACAAGTTGAGNAAGCTCATCAAAACCCAGAGGAATCTCAGTTTGTGAG 1800
Qy 1801 TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 1860
Db 1801 TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCA 1860
Qy 1861 AGAGGATCAAG 1920
Db 1861 AGAGGATCAAG 1920
Qy 1921 TTTTAACTGAGATGAGAGCAACTTGTATGATCGATATCGATATCGATATCGATATCGATATCGAT 1980
Db 1921 TTTTAACTGAGATGAGAGCAACTTGTATGATCGATATCGATATCGATATCGATATCGATATCGAT 1980
Qy 1981 CTACTATCCAAAACTTATCAATAAAACGTTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCCAAAACTTATCAATAAAACGTTTGTGCGTTGTTCTCC 2032

RESULT 6

AAS08537
ID AAS08537 standard; cDNA; 2041 BP.

AC AAS08537;

XX 23-OCT-2001 (first entry)

XX DNA encoding anaphylactic antigen Ara h 1.

XX Ara h 1; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;
allergy; mast cell; basophil; mouse; ss.

XX Mus sp.

PH	Key	Location/Qualifiers	Qy	241	GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACACTGGCACCACCAACCA	300
FT	CDS	50..1930	Dd	241		
FT		/*tag= a				
FT		/transl_except= (pos:902..904, aa:Ala)	Qy	301	ACGTTCCCTCCAGGGGAGCGGACACGTTGGCCGCAACCCGGAGACTACGATGATGACCG	360
FT		/product= "Peptide antigen Ara h 1"	Dd	301		
XX						
PN	W0200140264-A2.		Qy	361	CCGTCAACCCCGAAGAGAGGAGCGCGATGGGACCACTGGGACCGAGCTGGAGGGAGCGTGA	420
XX			Dd	361		
XX	07-JUN-2001.		Dd	361	CCGTCAACCCCGAAGAGAGGAGCGCGATGGGACCACTGGGACCGAGCTGGAGGGAGCGTGA	420
XX	06-DEC-2000; 2000WO-US033124.		Qy	421	AAGAGAAGAAAGACTGGAGACAAACCAAGAGAAGATTGGAGCGGACCAAGTTCATCAGCAGCC	480
PR	06-DEC-1999; 99US-0045294.		Dd	421		
PR	23-JUN-2000; 2000US-0213765P.					
PR	27-SEP-2000; 2000US-0235797P.		Qy	481	ACGGAAGAAAGACTGGAGACAAACCAAGAGAAGATTGGAGCGGACCAAGTTCATCAGCAGCC	480
XX			Dd	481		
PA	(PANA-) PANACEA PHARM LLC.		Qy	481	ACGGAAGAAAGACTGGAGACAAACCAAGAGAAGATTGGAGCGGACCAAGTTCATCAGTAGECCA	540
PA	(UYAR-) UNIV ARKANSAS.		Dd	481		
PA	(MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.		Qy	541	TGTGAGGGAAGAAACATCTCGGAACCAACCTTTCTACTTCCCGTCAAGGGCGTTTAGCAC	600
XX			Dd	541		
PI	Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;		Qy	601	CCGCTACGGGAACCAAAACGGTAGGATCCGGGTCCTGSCAGAGGTTTGACCAAAAGGTCAAG	660
XX	WPI: 2001-381378/40.		Dd	601		
DR	P-PSDB; AAU04706.		Qy	661	GCAGTTTCAGAAATCTCCAGNAATCAGCGTATTGTGCGAGATCGAGGCCCAACCTAACACTCT	720
XX			Dd	661		
CC	Antigenic fragments useful for reducing anaphylactic risk and reducing		Qy	721	TGTTCTTCCCAAGCAGCTGATGCTGATTAACATCTTGTATTCCAGCAAGGGCAAGCCAC	780
CC	the severity and/or number of allergic symptoms in individuals sensitive		Dd	721		
CC	to antigens, have reduced ability to bind Immunoglobulin E.		Qy	781	CGTGACCGTAGCAAAATGGCAATAACAGAAAGAGCTTTAAATCTTTGACGAGGCCCATGCAC	840
CC	Disclosure; Fig 9; 10pp; English.		Dd	781		
CC			Qy	841	CAGAAATCCATCCGGTTTCAATTCCTTACATCTTGAACCCGCATGACACCAAGACCTCAG	900
CC	The sequence represents the coding sequence of anaphylactic antigen Ara h		Dd	841		
CC	1. Ara h 1 is an anaphylactic antigen (A), which was used to design		Qy	901	AGTAGCTAAATCTCCATGCCCTTAAACACCCCGCCAGTTTGAAGATTCTTCCCGGC	960
CC	antigenic peptides having a reduced ability to bind immunoglobulin E		Dd	901		
CC	(Ige) as compared with the intact (A), or having a sequence substantially		Qy	961	GAGCAGCCGAGACCAATCATCTTACATCTTGAACCCGCATGACACCAAGACCTCAG	1020
CC	identical to a portion of sequence of an antigen that includes at least		Dd	961		
CC	one Ige binding site, where at least one Ige binding site of the peptide		Qy	1021	CITCAATCGGAAATTCATGAGNATCGGAGGTCCTGTTAGAGAGAAATCGCAGAGGTGA	1080
CC	is altered. The antigenic peptides are used in a composition which is		Dd	1021		
CC	useful for reducing risk or severity of allergic reaction to an antigen.		Qy	1081	GCAAGAGGAGAGAGGCGCAGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGAGT	1140
CC	This is done by identifying an individual at risk of allergic reaction to		Dd	1081		
CC	an antigen by identifying prior display of allergic symptoms when exposed		Qy	1141	GATAGTCAAAAGTGTCAAAGAGACGTTTGAAGAACTTACTTAAGCAGCTTAAATCCGTCCTC	1200
CC	to the antigen, or a familial relationship with an individual who		Dd	1141		
CC	previously displayed allergic symptoms when exposed to the antigen.		Qy	1201	AAAGAAAGGCTCCGAGAGAGGAGATATCACCACCAATCACTTGAGAGAGGCGGA	1260
CC	Following this an antigen-specific Ige present on one or more mast cells		Dd	1201		
CC	or basophils in the individual's serum is identified. The individual is		Qy	1261	GCCCGATCTTTCTAAACAATTTGGGAAAGTTATTGAGGTGAAGCCAGACAAGAAAGACCC	1320
CC	then contacted with a peptide corresponding to a portion of the antigen,		Dd	1261		
CC	which is selected, formulated, and delivered so that binding of the		Qy	1321	CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT	1380
CC	peptide to antigen-specific Ige is reduced as compared with Ige binding		Dd			
CC	of intact antigen. The composition is also useful for treating and		Qy			
CC	preventing allergic reactions		Dd			
XX	Sequence 2041 BP; 637 A; 473 C; 530 G; 401 T; 0 U; 0 Other;		Qy			
SQ			Dd			
	Query Match	100.0%; Score 2032; DB 4; Length 2041;				
	Best Local Similarity	100.0%; Pred. No. 0;				
	Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG	60			
Dd	1	AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG	60			
Qy	61	GGTTTCTCCACTGATGCTGTGTCTAGGATCCCTTGTCTGGCTTCAGTTTCTGCAACGCA	120			
Dd	61	GGTTTCTCCACTGATGCTGTGTCTAGGATCCCTTGTCTGGCTTCAGTTTCTGCAACGCA	120			
Qy	121	TGCCAAGTATACCTTACCAGAAAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA	180			
Dd	121	TGCCAAGTATACCTTACCAGAAAGAAACAGAGAACCCCTGCGCCAGAGGTGCCTCCA	180			
Qy	181	GAGTCTGCAACAGGAACCGATGACCTTGAAGCAAAAGGATCGAGTCTGCTGCACCAA	240			
Dd	181	GAGTCTGCAACAGGAACCGATGACCTTGAAGCAAAAGGATCGAGTCTGCTGCACCAA	240			

QY 1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGGAAGGTCCTCTTCAATTTTGAAGGC 1920
 DB 1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGGAAGGTCCTCTTCAATTTTGAAGGC 1920

QY 1921 TTTTAACTGA 1930
 DB 1921 TTTTAACTGA 1930

RESULT 9
 AAT76612
 ID AAT76612 standard; cDNA to mRNA; 1949 BP.
 XX AC
 XX AC
 DT 17-OCT-2003 (revised)
 DT 29-DEC-1997 (first entry)
 XX DE
 XX DE
 XX Peanut allergen Ara hi cDNA clone P17.
 KW Peanut; seed storage protein; allergen; allergy; hypersensitivity;
 KW vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;
 KW ELISA; analysis; Ara hi; ds.
 XX Arachis hypogaea; strain Flurunner.
 XX Key Location/Qualifiers
 FT CDS 3..1847
 FT /*tag= a
 FT sig_peptide 3..68
 FT /*tag= b
 FT mat_peptide 69..1844
 FT /*tag= c
 FT polyA_signal 1918..1923
 FT /*tag= d
 XX WO9724139-A1.
 PN 10-JUL-1997.
 XX 23-SEP-1996; 96WO-US015222.
 XX 29-DEC-1995; 95US-0009455P.
 PR 04-MAR-1996; 96US-00610424.
 XX (UYAR-) UNIV ARKANSAS.
 PA Burks AW, Helm RM, Cockrell G, Stanley JS, Bannon GA;
 PI WPI; 1997-363453/33.
 XX P-PSDB; AAW22149.
 XX Peanut allergens Ara hi and Ara hII - used for vaccination and in two-
 PT site monoclonal antibody based ELISA.
 XX Claim 31; Page 183-185; 354pp; English.
 PS This cDNA clone, designated p17, codes for the major peanut allergen Ara
 CC hi (AAW22149), which has multiple IgE binding epitopes (see AAW24165-87).
 CC It was amplified from peanut seed cDNA using a primer (see AAT76616)
 CC based on an isolated Ara hi peptide (see AAW24206). The sequence shows
 CC significant homology with the vicilin family of seed storage proteins of
 CC other legumes. The gene is capable of producing a protein product in
 CC prokaryotic cells that is recognised by serum IgE from a large proportion
 CC of individuals with peanut hypersensitivity. Ara hi and Ara hII (see
 CC AAW24164) can be used to raise monoclonal antibodies which are used in a
 CC specific two-site Mab ELISA for the detection of Ara hi or Ara hII
 CC (claimed). IgE-binding Ara antigen epitopes may be used in vaccines to
 CC protect against allergic reactions to peanut allergens, e.g. anaphylactic
 CC shock. (Updated on 17-OCT-2003 to standardise OS field)
 XX Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;
 SQ

Query Match 86.2%; Score 1752.4; DB 2; Length 1949;
 Best Local Similarity 95.0%; Pred. No. 0;
 Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;

QY 48 CAATGAGAGGAGGGTTTCTCCACTGATGTGTGTGTAGGATCTCTTGTCTGCTTCAAG 107
 DB 1 CAATGAGAGGAGGGTTTCTCCACTGATGTGTGTGTGTGGATCTCTTGTCTGCTTCAAG 60

QY 108 TTTTCTCAACGCATGCAAGTCATCCTTTACCAGAGAAGAAACAGAGAAACCCCTGCCGCC 167
 DB 61 TTTTCTCAACGCAGGGCCAGTCACCC-----TTACCGGAAAAACAGAGAACCCCTGCCGCC 114

QY 168 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCGGATGACTTTGAAGCAAAAGGCATGCCAGT 227
 DB 115 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCGGACGACTTTGAAGCAAAAGGCATGCCAGT 174

QY 228 CTGCTGACCAAGCTCGAGTATGATCTCTGTTGTGTGTATGATCTCTCGAGGACACACTG 287
 DB 175 CTGCTGACCAAGCTCGAGTATGATCTCTGTTGTGTGTATG-----ACACTG 222

QY 288 GCACCAACCAACGTTCCCTCCAGGAGCGGACACGTCGCCGCCAACCCCGAGACT 347
 DB 223 GCCTCACCAACCAACGTCACCTCTCCAGGAGCGGACACGTCGCCGCCAACCCCGAGACT 282

QY 348 ACGATGATGACCCCGCTCAACCCCGAAGAGAGGAGGCCGATGGGGACCACTGGAC 407
 DB 283 ACGATGATGACCCCGCTCAACCCCGAAGAGAGGAGGCCGATGGGGACCACTGGAC 342

QY 408 CGAGGAGCGTGAAGAGAAAGACTGGAGACAAACAAGAGAGATTTGGAGGCGACAA 467
 DB 343 CGAGGAGCGTGAAGAGAAAGACTGGAGACAAACAAGAGAGATTTGGAGGCGACAA 402

QY 468 GTCATCAGCAGCCACCGAAATTAAGCCCGAAGAGAGAGAGAACAGAGTGGGGAA 527
 DB 403 GTCATCAGCAGCCACCGAAATTAAGCCCGAAGAGAGAGAGAACAGAGTGGGGAA 462

QY 528 CACGAGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTTCTACTTCCCGTCAA 587
 DB 463 CACGAGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTTCTACTTCCCGTCAA 522

QY 588 GCGGTTTACACCCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTCGAGAGTTTG 647
 DB 523 GCGGTTTACACCCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTCGAGAGTTTG 582

QY 648 ACCAAGGTCAAGCAGTTTCAAGATCTCCAGAAATCACCGTATTGTGCAGATCGAGGCCA 707
 DB 583 ACCAAGGTCAAGCAGTTTCAAGATCTCCAGAAATCACCGTATTGTGCAGATCGAGGCCA 642

QY 708 AACCTAACACACTTGTGTTTCTTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGC 767
 DB 643 GACCTAACACACTTGTGTTTCTTCCCAAGCAGCTGATGCTGATAACATCTTGTATCCAGC 702

QY 768 AGGGCAAGCAGCCGCTAGCAGTAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 827
 DB 703 AAGGCAAGCAGCCGCTAGCAGTAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 762

QY 828 AGGGCAAGCAGCTAGCAGTAAATCTCCATGCCGTTTCAATTTCTTACATCTTGAACCCGCATGACA 887
 DB 763 AGGGCAAGCAGCTAGCAGTAAATCTCCATGCCGTTTCAATTTCTTACATCTTGAATCGACATGACA 822

QY 888 ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGCGCAGTTTGAGG 947
 DB 823 ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGCGCAGTTTGAGG 882

QY 948 ATTTCTTCGGGGCAGCAGCGAGACCAATCATCTACTTTCAGGAGGCTTCAGAGGAAATA 1007
 DB 883 ATTTCTTCGGGGCAGCAGCGAGACCAATCATCTACTTTCAGGAGGCTTCAGAGGAAATA 942

QY 1008 CGTTGAGAGCCGCTTCAATGCGGAATTCAAATGAGATACGAGAGGCTGCTGTTAGAGAGA 1067
 DB 943 CTTTGAGAGCCGCTTCAATGCGGAATTCAAATGAGATACGAGAGGCTGCTGTTAGAGAGA 1002

QY 1068 ATGCAGAGGTGACCAAGAGGAGAGAGGCGCAGAGCGATGCGAGTACTCGAGTAGTGAGA 1127
DB |||||||
QY 1003 ATGCAGAGGAGCAAGAGGAGAGAGGCGCAGAGCGATGCGAGTAGTG--- 1059
DB |||||||
QY 1128 ACAATCAAGAGAGTAGTCAAAAGTGTCAAAGGAGCAGCGTTGAAGAACTTACTAAGCAGC 1187
DB |||||||
QY 1060 ATATATGAGAGTAGTATGTCAAAGTGTCAAAGGAGCAGCGTTCAAGAACTTACTAAGCAGC 1119
DB |||||||
QY 1188 CTAATCCGTCTCAAAAGAAAGGCTCCGAAAGAGAGGAGATATCAACAAACCCCAATCAACT 1247
DB |||||||
QY 1120 CTAATCCGTCTCAAAAGAAAGGCTCC---GAAGAGGAAGATATCAACAAACCCCAATCAACT 1176
DB |||||||
QY 1248 TGAGAGAGGCGAGCCGATCTTTCAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307
DB |||||||
QY 1177 TGAGAGATGCGAGCCGATCTTTCAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1236
DB |||||||
QY 1308 ACAAGAGAAACCCCAAGCTTCAGGACCTGACATGATGTCTACCTGTGTAGAGATCAAAG 1367
DB |||||||
QY 1237 ACAAGAGAAACCCCAAGCTTCAGGACCTGACATGATGTCTACCTGTGTAGAGATCAAAG 1296
DB |||||||
QY 1368 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTATGCTGCTCGTCAACA 1427
DB |||||||
QY 1297 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTCATGCTGCTCGTCAACA 1356
DB |||||||
QY 1428 AAGGAACTGGAACCTTGAACCTGCTGCTCTAAGAAAGAGCAACACAGAGGGGACGCG 1487
DB |||||||
QY 1357 AAGGAACTGGAACCTTGAACCTGCTGCTCTAAGAAAGAGCAACACAGAGGGGACGCG 1416
DB |||||||
QY 1488 GGGAA-----GAAGAGGAGGAGCAAGCAAGAGGAGGGAAGTAACAGAGAGG 1538
DB |||||||
QY 1417 GGGAAACAGAGTGGGAAGAGAGGAGGAGAGATGAAGAGAGGAGGAGTAACAGAGAGG 1476
DB |||||||
QY 1539 TCGGTAGGTACACAGCGAGGTTGAAGAAAGCGCATGTGTTTCATCTGCCAGAGCTCATC 1598
DB |||||||
QY 1477 TCGGTAGGTACACAGCGAGGTTGAAGAAAGCGCATGTGTTTCATCTGCCAGAGCTCATC 1536
DB |||||||
QY 1599 CAGTAGCCATCAGCTTCTCCGAACCTCATCTGCTTGGCTTCGCTCAACGCTGAA 1658
DB |||||||
QY 1537 CAGTAGCCATCAGCTTCTCCGAACCTCATCTGCTTGGCTTCGCTCAACGCTGAA 1596
DB |||||||
QY 1659 ACAACACAGAACTTCTCTGCAAGGTGATAAGGACAAATGTGATAGACCAGATAGAAGC 1718
DB |||||||
QY 1597 ACAACACAGAACTTCTCTGCAAGGTGATAAGGACAAATGTGATAGACCAGATAGAAGC 1656
DB |||||||
QY 1719 AAGCGAAGGATTTAGCAATCCCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1778
DB |||||||
QY 1657 AAGCGAAGGATTTAGCAATCCCTGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1716
DB |||||||
QY 1779 AAGAGNATCTCACTTTGTGAGTGTGCTGCTCAATCTCAATCTCAATCTCCGCTCTC 1838
DB |||||||
QY 1717 AAGAGGAGTCTCACTTTGTGAGTGTGCTGCTCAATCTCAATCTCCGCTC----- 1765
DB |||||||
QY 1839 CTGAGAAAGAGTCTCTCGAAGAGAGGATCAAGAGGAGGAAAAACCAAGAGGGAAGGGTC 1898
DB |||||||
QY 1766 -----GTCTCTGAAAGAGAGGATCAAGAGGAGGAAAAACCAAGAGGGAAGGGTC 1815
DB |||||||
QY 1899 CACTCTTCAATTTGAAGCTTTTAACTGAGAAATGGAGGCAACTTGTATGATGAT 1958
DB |||||||
QY 1816 CACTCTTCAATTTTGAAGCTTTTAACTGAGAAATGGAGGAACTTGTATGATGAT 1875
DB |||||||
QY 1959 AATAAGATCAGCTTTTGTACTCTACTATCAAAAACCTTATCAATAAATAAAAACGTTTG 2018
DB |||||||
QY 1876 AATAAGATCAGCTTTTGTAACTTACTATCAAAAACCTTATCAATAAATAAAAACGTTTG 1935
DB |||||||
QY 2019 TGGGTTGTTTCTCC 2032
DB |||||||
QY 1936 TGGGTTGTTTCTCC 1949
DB |||||||

RESULT 10
ABX70604
ID ABX70604 standard; cDNA; 1949 BP.
XX

AC ABX70604;
XX
DT 26-MAR-2003 (first entry)
XX
DE Peanut Ara h1 cDNA clone P17.
XX
KW Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site;
XX anaphylactic food allergen; antiallergenic; vaccine; wound healing.
OS Arachis hypogaea.
PN WO200274250-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002WO-US009108.
XX
PR 16-MAR-2001; 2001US-0276822P.
PR 18-MAR-2002; 2002US-00276822.
XX
PA (PANA-) PANACEA PHARM.
PI Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
PI Rabjohn PA, Shin DS, Stanley JS;
XX
XX WPI; 2003-018765/01.
DR P-PSDB; ABU52413.
XX
XX New modified anaphylactic food allergen, useful for preventing or
XX treating allergic reactions associated with e.g. anaphylactic allergens.
XX
XX Example 3; Fig 11; 300pp; English.
XX
XX The invention relates to a modified anaphylactic food allergen has an
XX amino acid sequence that is substantially identical to that of natural
XX anaphylactic food allergen, except for a cysteine residue that has been
XX modified so that it cannot participate in the disulphide bond. The
XX modification may also comprise mutation of the IgE binding sites to
XX reduce allergenicity. Also included are: (1) a method of making a
XX modified anaphylactic food allergen; (2) a nucleotide molecule encoding
XX or for causing a site specific mutation in the modified anaphylactic food
XX allergen; (3) a transgenic plant or animal expressing the modified
XX anaphylactic food allergen; (4) a method of treating an individual by
XX reducing the clinical response to a natural anaphylactic food allergen;
XX and an isolated fragment of peanut allergen Ara h 1. The modified
XX anaphylactic food allergen is useful for preventing or treating allergic
XX reactions associated with any natural allergen such as food, insect,
XX rubber or preferably anaphylactic allergens. It is also useful for
XX treating wounds in mammals such as bovine, canine, feline, caprine,
XX ovine, porcine, murine or equine species. The present sequence is a cDNA
XX encoding a peanut allergen (e.g. Ara h1, h2 or h3)
SQ
Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;
Query Match 86.2%; Score 1752.4; DB 8; Length 1949;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;
QY 48 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTGTAGGATCCTTGTCTGGCTTCAG 107
DB 1 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTGTGGATCCTTGTCTGGCTTCAG 60
QY 108 TTTTGCACGCGATGCCAGTCATCCTTACAGAGAAACAGAGAACCCCTGCCGCC 167
DB 61 TTTTGCACGCGAGGCCAAGTCACC-----TTACCGGAAAAACAGAGAACCCCTGCCGCC 114
QY 168 AGAGGTGCCCTCCAGAGTTGTCAACAGAGAACCGGATGACTTTGAAGCAAAAGCGAGT 227
DB 115 AGAGGTGCCCTCCAGAGTTGTCAACAGAGAACCGGACGACTTTGAAGCAAAAGCGAGT 174
QY 228 CTCGCTGCACCAAGCTCGAGTATGATCTCTCGTTGTGTCTATGATCTCTCGAGGACACTG 287
DB |||||||


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XX 28-DEC-2004.
XX PF 13-NOV-1998; 98US-00191593.
XX PR 29-DEC-1995; 95US-0009455P.
XX PR 23-SEP-1996; 96US-00717933.
XX PA (UYAR-) UNIV ARKANSAS.
XX PI Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX DR WPI; 2005-045982/05.
XX DR P-PSDB; ADV97606.
XX PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
XX PT obtaining diagnostics with optimal concentrations of each allergen, for
XX PT developing panels of mixtures of recombinant allergens, and in
XX PT immunotherapy.
XX PS Claim 2; SEQ ID NO 4; 141pp; English.
XX CC This invention relates to a novel isolated nucleic acid molecule encoding
XX CC the peanut allergen Ara h 1 that has been identified in patients with
XX CC atopic dermatitis. Specifically, it refers to a monoclonal antibody
XX CC enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the
XX CC peanut allergens, where the monoclonal antibodies have specificity for a
XX CC selected peanut allergen antigen. The present invention also describes
XX CC hybridomas that produce two-site monoclonal antibodies specific for a
XX CC peanut allergen that can be used in an ELISA to detect and determine the
XX CC concentration of a specific peanut allergen in a food product or in food
XX CC processing. Furthermore, it provides an expression vector and the
XX CC isolated nucleic acid or its fraction can include a diagnostic label.
XX CC Accordingly, these nucleic acids are useful for obtaining diagnostics
XX CC with optimal concentrations of each allergen or for developing panels of
XX CC mixtures of large numbers of recombinant allergens such that it can be
XX CC used in immunotherapy for the treatment of food hypersensitivity
XX CC reactions. This polynucleotide sequence is the peanut Ara h 1 allergen
XX CC cDNA (P17 clone) of the invention.
XX SQ Sequence 1949 BP; 599 A; 455 C; 517 G; 378 T; 0 U; 0 Other;
Query Match 86.2%; Score 1752.4; DB 14; Length 1949;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;
QY 48 CAATGAGAGGAGGGTTCTCCACTGATGCTGTGTCTAGGGATCCTTGTCTGGCTTCAG 107
DB 1 CAATGAGAGGAGGGTTCTCCACTGATGCTGTGTCTGGGATCCTTGTCTGGCTTCAG 60
QY 108 TTTCTGCAACGATGCCAAGTGTGCAACAGGAACCGGATGACTTGAAGCAAAAGGCAATGCGAGT 167
DB 61 TTTCTGCAACGCGCAAGTACC-----TTACCGGAAACAGAGAACCCTTCGCGCC 114
QY 168 AGAGGTGCTCCAGAGTTGTCAACAGGAACCGGATGACTTGAAGCAAAAGGCAATGCGAGT 227
DB 115 AGAGGTGCTCCAGAGTTGTCAACAGGAACCGGACGACTTGAAGCAAAAGGCAATGCGAGT 174
QY 228 CTCGCTGCACCAAGCTCGAGTATGATCTCCTGTGTGTCTATGATCTCTCGAGGACACACTG 287
DB 175 CTCGCTGCACCAAGCTCGAGTATGATCTCCTGTGTGTGTATG-----ACACTG 222
QY 288 GCACCAACCAACGTTTCCCTCCAGGGAGCGGACAGCTGCGCGCCCAACCCGGAGACT 347
DB 223 GCGCCACCAACCAACGTTCACTCCAGGGAGCGGACAGCTGCGCGCCCAACCCGGAGACT 282
QY 348 ACCGATGATGACCGCGTCAACCCCGGAGAGGAAGGAGCGCGATGGGGACCAAGCTGGAC 407
DB 283 ACCGATGATGACCGCGTCAACCCCGGAGAGGAAGGAGCGCGATGGGGACCAAGCTGGAC 342
QY 408 CGAGGGAGCGTGAAGAGGAAGAGACTGGAGACAAACCAAGAGAGATTTGGAGCGCAACAA 467
DB 343 CGAGGGAGCGTGAAGAGGAAGAGACTGGAGACAAACCAAGAGAGATTTGGAGCGCAACAA 402
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QY 468 GTCATCAGCAGCCACGGAATAAGCCCGAAGGAAGAGAGAAACAAGAGTGGGAA 527
DB |||||
DB 403 GTCATCAGCAGCCACGGAATAAGCCCGAAGGAAGAGAGAAACAAGAGTGGGAA 462
QY 528 CACCAGGTAGCATGTGAGGAAGAAACATCTCGGAACAAACCCCTTTCTACTTCCCGTCAA 587
DB |||||
DB 463 CACCAGGTAGCATGTGAGGAAGAAACATCAGGAAACAACCCCTTTCTACTTCCCGTCAA 522
QY 588 GCGGTTTATGACACCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGCAGAGTTTG 647
DB |||||
DB 523 GCGGTTTATGACACCCGCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGCAGAGTTTG 582
QY 648 ACCAAGGTACAGGCAAGTTTTCAGATCTCCAGATCACCGTATTTGTCAGATCAGGCGCA 707
DB |||||
DB 583 ACCAAGGTACAGGCAAGTTTTCAGATCTCCAGATCACCGTATTTGTCAGATCAGGCGCA 642
QY 708 AACCTAACACTCTTGTCTTCCCAAGCAGCTGATCTGATACATCCTTTGTTATCCAGC 767
DB |||||
DB 643 GACCTAACACTCTTGTCTTCCCAAGCAGCTGATCTGATACATCCTTTGTTATCCAGC 702
QY 768 AAGGCAAGCCACCGTAGCAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 827
DB |||||
DB 703 AAGGCAAGCCACCGTAGCAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTGACG 762
QY 828 AGGCCATGCACCTCAGAAATCCCATCCGTTTCAATTTCTTACATCTTTGMAACCGCATGACA 887
DB |||||
DB 763 AGGCCATGCACCTCAGAAATCCCATCCGTTTCAATTTCTTACATCTTTGAAATCGACATGACA 822
QY 888 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCCTTAACACACCCGGCAGTTTGAGG 947
DB |||||
DB 823 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCCCTTAACACACCCGGCAGTTTGAGG 882
QY 948 ATTTCTTCCGGCAGCAGCCGAGACCAATCATCTTCTTACATCTTTGMAACCGCATGACA 1007
DB |||||
DB 883 ATTTCTTCCGGCAGCAGCCGAGACCAATCATCTTCTTACATCTTTGMAACCGCATGACA 942
QY 1008 CGTTGAGGCGCCCTTCAATGCGGAATTCAAATGAGATACGAGGCTGTTTGAAGAGA 1067
DB |||||
DB 943 CTTTGAGGCGCCCTTCAATGCGGAATTCAAATGAGATACGAGGCTGTTTGAAGAGA 1002
QY 1068 ATGAGGAGGTGAGCAAGAGGAGAGGCGCAGAGCGATGGAGTACTCGGAGTAGTGAGA 1127
DB |||||
DB 1003 ATGAGGAGGAGAGCAAGAGGAGAGGAGGCGAGCGAGTACTCGGAGTAGTG--- 1059
QY 1128 ACATGAAGAGTAGTAGTCAAAGTGTCAAAGGAGCACGTTGAGAACTTACTTAAGCAGC 1187
DB |||||
DB 1060 ATAATGAAGAGTAGTAGTCAAAGTGTCAAAGGAGCACGTTCAAGAACTTACTTAAGCAGC 1119
QY 1188 CTAATCCGCTCTCAAAGAAAGGCTCCGAAGAGAGGAGAGATATCAACCAACCAATCAACT 1247
DB |||||
DB 1120 CTAATCCGCTCTCAAAGAAAGGCTCC---GAAGAGGAAGATATCAACCAACCAATCAACT 1176
QY 1248 TGAGAGAGGCGAGCCCGATCTTTCTAAACACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307
DB |||||
DB 1177 TGAGAGATGCGGAGCCCGATCTTTCTAAACACTTTGGGAGTTATTTGAGGTGAAGCCAG 1236
QY 1308 ACAGAAAGAACCCCGAGCTTCAGGACCTGGACATGATGTCTACCTGTGTAGAGATCAAG 1367
DB |||||
DB 1237 ACAAGAAAGAACCCCGAGCTTCAGGACCTGGACATGATGTCTACCTGTGTAGAGATCAAG 1296
QY 1368 AAGGAGCTTTGATGCTCCACACTCTCAACTCAAAGGCCATGGTTATCTGCTCGTCAACA 1427
DB |||||
DB 1297 AAGGAGCTTTGATGCTCCACACTTCAACTCAAAGGCCATGGTTCATCGTCTGTCACACA 1356
QY 1428 AAGGAACTGGAAACTTTGAACTCGTGGCTGTAAAGAAAGAGCAACCAACAGAGGGGACGC 1487
DB |||||
DB 1357 AAGGAACTGGAAACTTTGAACTCGTAGCTGTAAAGAAAGAGCAACCAACAGAGGGGACGC 1416
QY 1488 GGGAA-----GAAGAGGAGGACGAGACCAAGAGAGGAGGGAAGTAACAGAGAGG 1538
DB |||||
DB 1417 GGGAAACAGAGTGCGGAAGAGAGGAGGAAGATGAAGAGAGGAGGGAAGTAACAGAGAGG 1476
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QY 1539 TGGTAGGTACACAGCGAGGTGAAGGAAGCGATGTGTTTCATCATGCGACGACTCATC 1598
Db 1477 TCGTAGGTACACAGCGAGGTGAAGGAAGCGATGTGTTTCATCATGCGACGACTCATC 1536
QY 1599 CAGTAGCCATCAAGCGTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAA 1658
Db 1537 CAGTAGCCATCAAGCGTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACGCTGAAA 1596
QY 1659 ACAACACACAGAATCTTCTTGCAGGTGATAGGACAAATGTAGACCAATGATAGAGAAGC 1718
Db 1597 ACAACACACAGAATCTTCTTGCAGGTGATAGGACAAATGTAGACCAATGATAGAGAAGC 1656
QY 1719 AAGCGAAGGATTTAGCAATCCCTGGGTCCGGAAGTTGAGAAGCTCATCAAAAACC 1778
Db 1657 AAGCGAAGGATTTAGCAATCCCTGGGTCCGGAAGTTGAGAAGCTCATCAAAAACC 1716
QY 1779 AGAAGGAATCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCCGTC 1838
Db 1717 AGAGGAGTCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCCGTC 1765
QY 1839 CTGAGAAAGAGTCTCTCGAAGAGAGGATCAAGAGGAGGAAACCAGGAGGGAAGGTC 1898
Db 1766 -----GTCTCTGAAAAGAGGATCAAGAGGAGGAAACCAGGAGGGAAGGTC 1815
QY 1899 CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTATGATCGAT 1958
Db 1816 CACTCCTTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTATGATCGAT 1875
QY 1959 AATAAGATCAAGCTTTTGTACTCTACTATCCAAAACCTTATCAATAAATAAAGCTTTG 2018
Db 1876 AATAAGATCAAGCTTTTGTAACTACTATCTATCCAAAACCTTATCAATAAATAAAGCTTTG 1935
QY 2019 TGGTTGTTTCTCC 2032
Db 1936 TGGTTGTTTCTCC 1949

RESULT 12
ADG27463
ID ADG27463 standard; cDNA; 1949 BP.
XX AC ADG27463;
XX DT
XX 26-FEB-2004 (first entry)
XX DE Peanut Ara h1 cDNA clone P17.
XX KW Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3;
XX KW glycinin A2B1a; Jug n1; antiallergic; vulnerary;
XX KW anaphylactic food allergen; IgE; allergy; wound.
XX OS
XX Arachis hypogaea.
XX PN US2003202980-A1.
XX PD
XX 30-OCT-2003.
XX PF 18-MAR-2002; 2002US-00100303.
XX PR 29-DEC-1995; 95US-0009455P.
XX PR 23-SEP-1996; 96US-00717933.
XX PR 31-JAN-1998; 98US-0073283P.
XX PR 13-FEB-1998; 98US-0074590P.
XX PR 13-FEB-1998; 98US-0074624P.
XX PR 13-FEB-1998; 98US-0074633P.
XX PR 29-JUN-1998; 98US-00106872.
XX PR 27-AUG-1998; 98US-00141220.
XX PR 13-NOV-1998; 98US-00191593.
XX PR 29-JAN-1999; 99US-00240557.
XX PR 29-JAN-1999; 99US-00241101.
XX PR 11-FEB-1999; 99US-00248673.
XX PR 11-FEB-1999; 99US-00248674.
XX PR 02-MAR-1999; 99US-0122450P.
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PR 02-MAR-1999; 99US-0122452P.
PR 02-MAR-1999; 99US-0122560P.
PR 02-MAR-1999; 99US-0122565P.
PR 02-MAR-1999; 99US-0122566P.
PR 11-MAR-1999; 99US-00267719.
PR 28-JAN-2000; 2000US-00494096.
PR 16-MAR-2001; 2001US-0276822P.
XX (CAPL/) CAPLAN M J.
PA (SOSI/) SOSIN H B.
PA (SAMP/) SAMPSON H.
PA (BANN/) BANNON G A.
PA (BURK/) BURKS A W.
PA (COCK/) COCKRELL G.
PA (COMP/) COMPADRE C M.
PA (CONV/) CONNAUGHTON C.
PA (HELM/) HELM R M.
PA (KING/) KING N E.
PA (KOPP/) KOPPER R A.
PA (MALE/) MALEKI S J.
PA (RABJ/) RABJOHN P A.
PA (SHIN/) SHIN D S.
PA (STAN/) STANLEY J S.
XX Caplan MJ, Sosin HB, Sampson H, Bannon GA, Burks AW, Cockrell G;
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
PI Rabjohn PA, Shin DS, Stanley JS;
XX WPI; 2003-875632/81.
DR P-PSDB; ADG27465.
XX New modified anaphylactic food allergen comprising a cysteine residue
PT which has been modified so that it cannot participate in the disulfide
PT bond, useful for treating allergic reactions or wounds.
XX Example 4; SEQ ID NO 6; 194pp; English.
XX The invention relates to a modified anaphylactic food allergen whose
CC amino acid sequence is substantially identical to that of a natural
CC anaphylactic food allergen. The natural anaphylactic food allergen
CC includes at least one cysteine residue that participates in a disulphide
CC bond when the natural anaphylactic food allergen is in its native
CC conformation, except that the cysteine residue has been modified so that
CC it cannot participate in the disulphide bond. Also included are a method
CC of making a modified anaphylactic food allergen, a nucleotide molecule
CC encoding a modified anaphylactic food allergen defined above, a
CC nucleotide molecule for causing a site specific mutation in a gene
CC encoding a natural anaphylactic food allergen, a transgenic plant or
CC animal expressing a modified anaphylactic food allergen defined above, a
CC method of treating an individual by reducing the clinical response to a
CC natural anaphylactic food allergen by administering a modified
CC anaphylactic food allergen and an isolated fragment of peanut allergen
CC Ara h 1, comprising at least 10 consecutive amino acids of ADG27464 or
CC ADG27465. About 10-17% of the amino acids have been modified in at least
CC one IgE epitope or all the IgE epitopes recognised when the natural
CC anaphylactic food allergen is contacted with serum IgE from individual(s)
CC allergic to the natural anaphylactic food allergen. The invention
CC discloses peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding
CC cDNAs), Soybean Glycinin A2B1a and IgE-binding epitopes of the English
CC walnut allergen Jug n1. The modified anaphylactic food allergen can be
CC used for treating allergic reactions or wounds. The present sequence
CC encodes a Peanut allergen of the invention.
XX SQ Sequence 1949 BP; 599 A; 456 C; 516 G; 378 T; 0 U; 0 Other;
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Query Match 86.2%; Score 1750.8; DB 10; Length 1949;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 1893; Conservative 0; Mismatches 47; Indels 54; Gaps 6;
QY 48 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTAGGATCCTTGTCTGGCTTCAG 107
Db 1 CAATGAGAGGAGGGTTTCTCCACTGATGCTGTGTAGGATCCTTGTCTGGCTTCAG 60
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Db 1358 AAGAACTCGAAACCTTGAACCTGCTAGCTGTAAAGAAAAGAGCAACAAACAGAGGGGACGGC 1417
QY 1488 GGGAA-----GAAGAGGAGACGAAGACGAAGAGGGGGAAGTAACAGAGAGGT 1539
Db 1418 GGGACAAAGCTGCAAGAGAGGACGAAGACTAAGAGAGGGGGAAGTAACAGAGAGGT 1477
QY 1540 GGTAGGTACACAGCAGGTTGAAGGAAGGCGATGTGTCATCATGCCAGCAGCTCATCC 1599
Db 1478 GCGTAGGTACACAGCAGGTTGAAGGAAGGCGATGTGTCATCATGCCAGCAGCTCATCC 1537
QY 1600 AGTAGCCATCAGCTTCCCTCCGAACCTCATCTGCTTGGCTTCGGGTATCAACGCTCAAAA 1659
Db 1538 AGTAGCCATCAGCTTCCCTCCGAACCTCATCTGCTTGGCTTCGGGTATCAACGCTCAAAA 1597
QY 1660 CAACCAAGAAATCTCTTTCAGGTGATTAAGGACAATGTGATAGACCAGATAGAGAAGCA 1719
Db 1598 CAACCAAGAAATCTCTTTCAGGTGATTAAGGACAATGTGATAGACCAGATAGAGAAGCA 1657
QY 1720 AGCGAAGGATTTAGCAATTCCTCGGTGCGGTGAACAAAGTTGAGAAGCTCATCAAAAACCA 1779
Db 1658 AGCGAAGGATTTAGCAATTCCTCGGTGCGGTGAACAAAGTTGAGAAGCTCATCAAAAACCA 1717
QY 1780 GAAGGAATCTCACTTGTGAGTCTCGTCTCAATCTCAATCTCAATCTCCGTCGTCTCC 1839
Db 1718 GAGGAGTCTCACTTGTGAGTCTCGTCTCAATCTCCGTC----- 1759
QY 1840 TGAGAAAGAGTCTCTCTGAGAAAGAGTCAAGAGGAGGAAACCAAGGAGGGAAGGTCC 1899
Db 1760 -----GTCTCTGAAAGAGAGTCAAGAGGAGGAAACCAAGGAGGGAAGGTCC 1810
QY 1900 ACTCCTTTCAATTTTGAAGGCTTTAACTGAGAAATGGAGGAAACTTTGTTATGTATCCATA 1959
Db 1811 ACTCCTTTCAATTTTGAAGGCTTTAACTGAGAAATGGAGGAAACTTTGTTATGTATCCATA 1870
QY 1960 ATAAGATCAGCTTTGTACTCTACTATCAAAAACCTTATCAATAATAAAACGTTTGT 2019
Db 1871 ATAAGATCAGCTTTGTACTCTACTATCAAAAACCTTATCAATAATAAAACGTTTGT 1930
QY 2020 GCGTTGTTTCTCC 2032
Db 1931 GCGTTGTTTCTCC 1943

RESULT 14
ADV97605
ID ADV97605 standard; cDNA; 1340 BP.
AC ADV97605;
XX
XX
XX
DT 10-MAR-2005 (first entry)
XX
XX Peanut Ara h 1 allergen alpha (clone 5 Ala) cDNA.
DE
XX
XX allergen; atopic dermatitis; diagnostic; immunotherapy;
KW immediate type hypersensitivity; Ara h 1; dermatological; antiallergic;
KW immunosuppressive; antibody engineering; gene; ss.
XX
XX Arachis hypogaea.
OS
XX
XX
PH Key Location/Qualifiers
CDS 231..1238
FT /*tag= a
FT /product= "Ara h 1 (clone 5 Ala) protein"
FT
FT
PN US6835824-B1.
XX
XX
PD 28-DEC-2004.
XX
XX 13-NOV-1998; 98US-00191593.
XX
XX 29-DEC-1995; 95US-0009455P.
PR 23-SEP-1996; 96US-00717933.
XX

PA (UYAR-) UNIV ARKANSAS.
XX
PI Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX
DR WPI: 2005-045982/05.
DR P-PSDB; ADV97604.
XX
PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
PT obtaining diagnostics with optimal concentrations of each allergen, for
PT developing panels of mixtures of recombinant allergens, and in
PT immunotherapy.
XX
PS Disclosure; Col 75-78; 141pp; English.
XX
CC This invention relates to a novel isolated nucleic acid molecule encoding
CC the peanut allergen Ara h 1 that has been identified in patients with
CC atopic dermatitis. Specifically, it refers to a monoclonal antibody
CC enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the
CC peanut allergens, where the monoclonal antibodies have specificity for a
CC selected peanut allergen antigen. The present invention also describes
CC hybridomas that produce two-site monoclonal antibodies specific for a
CC peanut allergen that can be used in an ELISA to detect and determine the
CC concentration of a specific peanut allergen in a food product or in food
CC processing. Furthermore, it provides an expression vector and the
CC isolated nucleic acid or its fraction can include a diagnostic label.
CC Accordingly, these nucleic acids are useful for obtaining diagnostics
CC with optimal concentrations of each allergen or for developing panels of
CC mixtures of large numbers of recombinant allergens such that it can be
CC used in immunotherapy for the treatment of food hypersensitivity
CC reactions. This polynucleotide sequence is the peanut Ara h 1 allergen
CC cDNA (clone 5 Ala) of the invention.
XX
SQ Sequence 1340 BP; 422 A; 296 C; 340 G; 282 T; 0 U; 0 Other;

Query Match 65.2%; Score 1324; DB 14; Length 1340;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1340; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 687 GTATTGTGAGATCGAGGCGCAACCTTAACACTCTTGTCTTCCCAAGCAGCTGATGCTG 746
Db 1 GTATTGTGAGATCGAGGCGCAACCTTAACACTCTTGTCTTCCCAAGCAGCTGATGCTG 60
QY 747 ATAACATCTCTGTTATCCAGCAAGGCAAGCCCTGACCTAGCAAAATGGCAATAACA 806
Db 61 ATAACATCTCTGTTATCCAGCAAGGCAAGCCCTGACCTAGCAAAATGGCAATAACA 120
QY 807 GAAAGAGCTTTAATCTTGAAGGCGCATGCACTCAGAAATCCCATCCGTTTCATTTCTCT 866
Db 121 GAAAGAGCTTTAATCTTGAAGGCGCATGCACTCAGAAATCCCATCCGTTTCATTTCTCT 180
QY 867 ACATCTTGAACCGCCATGACCAACCAACCTCAGAGTAGCTAAATCTCCATGCCGTTA 926
Db 181 ACATCTTGAACCGCCATGACCAACCAACCTCAGAGTAGCTAAATCTCCATGCCGTTA 240
QY 927 ACACACCCCGCCAGTTTGAAGGATTTCTTCCGGCGAGCAGCCGAGACCAATCATCTTCT 986
Db 241 ACACACCCCGCCAGTTTGAAGGATTTCTTCCGGCGAGCAGCCGAGACCAATCATCTTCT 300
QY 987 TGCAGGGCTTCAGCAGGAATAACGTTGGAGGCCCTTCAATCGGAATTCATAGATAC 1046
Db 301 TGCAGGGCTTCAGCAGGAATAACGTTGGAGGCCCTTCAATCGGAATTCATAGATAC 360
QY 1047 GGAGGGTGTGTTAGAAAGAAATGCAGAGGTGACGAAGGAGGAGGCGCAGGCGAT 1106
Db 361 GGAGGGTGTGTTAGAAAGAAATGCAGAGGTGACGAAGGAGGAGGCGCAGGCGAT 420
QY 1107 GGAGTACTCGGAGTAGTGAGAAACAATGAAGAGTAGTAGTCAAAAGTGTCAAAGGAGCAG 1166
Db 421 GGAGTACTCGGAGTAGTGAGAAACAATGAAGAGTAGTAGTCAAAAGTGTCAAAGGAGCAG 480
QY 1167 TTGAAGAACTTACTAAGCAGCGCTAAATTCGCTCTCAAAGAAAGGCTTCGAAGAGAGGAG 1226
Db 481 TTGAAGAACTTACTAAGCAGCGCTAAATTCGCTCTCAAAGAAAGGCTTCGAAGAGAGGAG 540


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QY 1227 ATATCACCAACCCCAATCAACTTGAGAGAAGCGGAGCCCGATCTTCTTAACAACATTTTGGGA 1286
DB 541 ATATCACCAACCCCAATCAACTTGAGAGAAGCGGAGCCCGATCTTCTTAACAACATTTTGGGA 600
QY 1287 AGTTATTGTAGGTGAAGCCAGACAAAGAAAGAACCCCGAGCTTCAGGACCTGGACATGATGC 1346
DB 601 AGTTATTGTAGGTGAAGCCAGACAAAGAAAGAACCCCGAGCTTCAGGACCTGGACATGATGC 660
QY 1347 TCACCTGTGTAGAGATCAAAAGNAGGAGCTTGTAGTCTCCACACTTCAACTCAAAAGGCCA 1406
DB 661 TCACCTGTGTAGAGATCAAAAGNAGGAGCTTGTAGTCTCCACACTTCAACTCAAAAGGCCA 720
QY 1407 TGGTTATTCGTCTGCTCAACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAAGAAAAG 1466
DB 721 TGGTTATTCGTCTGCTCAACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAAGAAAAG 780
QY 1467 AGCAACACAGAGGGGACGGCGGGAAGAAAGAGGAGGACGAAGACGAAGAGAGAGGGAA 1526
DB 781 AGCAACACAGAGGGGACGGCGGGAAGAAAGAGGAGGACGAAGACGAAGAGAGAGGGAA 840
QY 1527 GTAAACAGAGAGGTCGTAGGTACACAGGAGGAGTGAAGGAGGCGATGTTCTATCATGTC 1586
DB 841 GTAAACAGAGAGGTCGTAGGTACACAGGAGGAGTGAAGGAGGCGATGTTCTATCATGTC 900
QY 1587 CAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTA 1646
DB 901 CAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTA 960
QY 1647 TCAACGCTGAAAACCAACAGCAATCTTCTTGCAGGTGATAAGGACCAATGTGATAGCC 1706
DB 961 TCAACGCTGAAAACCAACAGCAATCTTCTTGCAGGTGATAAGGACCAATGTGATAGCC 1020
QY 1707 AGATAGAGAGCAGCAGCAAGGATTTAGCATTCCTGGTGGGTGACCAAGTTGAGAGC 1766
DB 1021 AGATAGAGAGCAGCAGCAAGGATTTAGCATTCCTGGTGGGTGACCAAGTTGAGAGC 1080
QY 1767 TCATCAAAAACCAAGAGGAATCTCAGTCTTGTGAGTGTCTGCTCAATCTCAATCTCAAT 1826
DB 1081 TCATCAAAAACCAAGAGGAATCTCAGTCTTGTGAGTGTCTGCTCAATCTCAATCTCAAT 1134
QY 1827 CTCGCTGCTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAACCAAG 1886
DB 1135 CTCGCTGCTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAACCAAG 1194
QY 1887 GAGGAGGCTCCACTCTCTTCAATTTTGAAGGCTTTAACTGAGATGAGGCAACTTG 1946
DB 1195 GAGGAGGCTCCACTCTCTTCAATTTTGAAGGCTTTAACTGAGATGAGGCAACTTG 1254
QY 1947 TTATGTATCGATAATAAGATCAGGCTTTTGTACTCTACTATCCAAAACCTTATCAATAA 2006
DB 1255 TTATGTATCGATAATAAGATCAGGCTTTTGTACTCTACTATCCAAAACCTTATCAATAA 1314
QY 2007 TAAAAAGCTTTGTGCGTTGTTCTCC 2032
DB 1315 TAAAAAGCTTTGTGCGTTGTTCTCC 1340
```

RESULT 15

ABS55196

ID ABS55196 standard; DNA; 1251 BP.

XX AC

XX AC ABS55196;

XX XX

DT 17-DEC-2002 (first entry)

DE XX

XX Glycine max (Soybean) var. Wasesuzunari gene #2.

XX DE

XX Soybean; Glycinin; atomic coordinate data; processability; soya protein;

XX KW

XX Wasesuzunari; protein co-ordinate data; gene; ds.

XX XX

OS Glycine max.

XX XX

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PH Key Location/Qualifiers
FT CDS 1..1251
FT /tag= a
FT /partial
FT /product= "Glycine max (Soybean) var. Wasesuzunari
FT protein #2"
FT /note= "This sequence lacks a stop codon"
XX XX
XX JP2002193996-A.
XX XX
XX 10-JUL-2002.
XX XX
XX 21-DEC-2000; 2000JP-00405097.
XX XX
XX 21-DEC-2000; 2000JP-00405097.
XX XX
XX (KYOU ) UNIV KYOTO.
XX XX
XX WP1; 2002-685438/74.
XX DR P-PSDB; ABG71269.
XX XX
XX Glycinin, beta-conglycinin and proglycinin, their crystal structures,
XX three dimensional coordinates, three dimensional structured and models
XX and their uses.
XX Disclosure; Page 1282-1283; 1298pp; Japanese.
XX PS
XX The present invention relates to a new Glycinin characterised by the
XX atomic coordinate data fully defined in the specification. The structure
XX can be used for improving processability of soya protein. The present
XX nucleic acid sequence encodes the Glycine max (Soybean) var. Wasesuzunari
XX protein #2, as described in the specification
XX XX
XX Sequence 1251 BP; 385 A; 304 C; 265 G; 297 T; 0 U; 0 Other;
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Query Match 20.1%; Score 408.4; DB 6; Length 1251;

Best Local Similarity 62.2%; Pred. No. 1.3e-109;

Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

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QY 562 GAACACCCCTTCTACTT---CCGTCAGGCGGTTTAGCACCGCTACGGGACCAAAA 618
DB 24 GAATAACCCCTTCTACTTTAGAAAGCTCTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 83
QY 619 CGGTAGGATCCGGGTCCTGCAGAGGTTTGACCAAGGTCAAGGCAGTTTCAGAAATCTCCA 678
DB 84 CGTGCATTCGTCTCTCCAGAGATTCACAAACGCTCCCACTTCCGAACTTCCG 143
QY 679 GAATACCGTATTTGTGAGATCGAGGCCAAACCTTAACACTCTTGTTCCTCCAGACGCG 738
DB 144 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCCCAACAACTCTTCTCCCCCAATGC 203
QY 739 TGATGCTGATAACATCTTGTATCCAGCAAGGCAAGCCACCGTGACCGTAGCAATGG 798
DB 204 TGACCGCGATTTCTCTCTCTTTGTCTTACGGGAGAGCCATATCTTACCTTGGTGAACAA 263
QY 799 CAATAACAGAAAGAGCTTTAATCTTCAAGGCGCCATGCACTCAGAAATCCCATCCGGTTT 858
DB 264 CGACGACAGAGACTCTACAACTTCCCTGCGATGCCAGAGAACTCCAGCTGGAAC 323
QY 859 CATTTCTCATCTTGAACCGCCATGACAAACCAAGACCTCAGAGTAGCTAAAATCTCCAT 918
DB 324 CACTTACTATTTGGTTAAACCCCTCACGACCAACCAAGAAATCTCAAAATAATCAAACTTGCAT 383
QY 919 GCCGTTTAACACACCGCCAGTTTGAGGATTTCTTCCCGCGGAGCGGAGCCAGCAATC 978
DB 384 ACCGTCACAAACACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 443
QY 979 ATCTACTTTCAGGGCTTCAGCAGGAATACGTTGGAGGCGGCTTCAATCGGAATTTCAA 1038
DB 444 GTCTACTTTCAGAGGCTTCAGCCATTAATTTCTAGAGACCTCTCTCATAGCAATTCGA 503
QY 1039 TGAGATACGGAGGCTGCTGTGTAGAGAGAAATGCAAGAGGTGAGCAAGAGGAGAGGCA 1098
DB 1039 TGAGATACGGAGGCTGCTGTGTAGAGAGAAATGCAAGAGGTGAGCAAGAGGAGAGGCA 1098
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Db      504 GGAGATAAACAGGGTTTTGTTGGAGAGGAGAGGAGCAGCAGCAAGAG----- 555
Qy      1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGATAGTCAAAAGTGTCAAA 1158
Db      556 -----GGAGTGATCGTGGAACTCTCAAA 578
Qy      1159 GGAGCAGGTTGAAGAACTTACTAAGCACGCTAATCCGTCCTCAAGAAAGGCTCCGAGA 1218
Db      579 GGAACAAATTCGGCAACTAGCAGAGCGTGCCAAATCTAGTTCAAGGAAACCAATTCCTC 638
Qy      1219 AGAGGGAGATATCACCAACCCAACTCAACTTGAGAGAGGCGGCGCGATCTTTCTAACAA 1278
Db      639 CGAAGATG-----AACCATTCACCTTGAGAGCGGCAACCCCATCTATTCCAAACAA 689
Qy      1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAAGAACCCCCAGCTTCAGGACCTGGA 1338
Db      690 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAAAACCCACAGCTTCGGGACTTGA 746
Qy      1339 CATGATGCTCACCTGTGTAGAGATCAAGAGAGGCTTTGATGCTCCACACTTCAACTC 1398
Db      747 TATCTTCCCTCAGTTCTGTGGATATCAACGAAGAGGCTTCCTTCTACCACTTCAATTC 806
Qy      1399 AAAGGCCATGGTTATCGTCGTCTCAACAAAGGAACCTGGAAACCTTGAACCTCGTGGCTGT 1458
Db      807 AAAGGCCATAGTACTAGTGTATTAATGAAGGAGATGCAAAACATTGAACCTTGTGGCAT 866
Qy      1459 AAGAAAGAGCAACAACAGAGGGGACGGCGGGAAGAAAGAGGAGGACGAAGACGAAGA 1518
Db      867 TAAAGAAACAACAACAGAAAGCAAGAAAGGAAGGAACCTTTG----- 909
Qy      1519 GGAGGGNAGTTAACAGAGAGGTGCGTAGGTACACAGCGAGGTTGAAGGAGGCGATGTGT 1578
Db      910 -----GAAGTGAAAGGTACAGAGCTGAATTTCTGAAGACCATGTATT 953
Qy      1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTCGAACTCCATCTGCTTGG 1638
Db      954 TGTAAATCCAGCAGCTTATCCATTGTGCTCAACGCTACCTCAAACTCAATTCCTTGC 1013
Qy      1639 CTTGCGTATCAACGCTGAACCAACCAAGAAATCTTCCTTGCAGGTGATAAGGACAATGT 1698
Db      1014 TTTTGGTATCAATGCTGAGAAACAACAGAGGAACTTCCTTGCAGGCGAGAAAGACAATGT 1073
Qy      1699 GATAGACCAGATAGAGAAAGCAAGCGAGGATTTAGCATTCCTGGGTCCGGTGCAACAAGT 1758
Db      1074 GGTAAAGCATAGAAGACAAGTGCAGGAGCTTGGCTCCCTGGGTCTGCACAAGATGT 1133
Qy      1759 TGAGAGCTCATCAAAACCCAGAGGAATCTCACTTTGTGAGTGTCTCGTCTCA 1812
Db      1134 TGAGAGGCTATTAAAGAGCAGAGGGGAATCCTACTTTGTGATGCTCAGCCTCA 1187
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Search completed: June 22, 2006, 11:35:24
Job time : 914.436 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 10443.4 Seconds
(without alignments)
10880.347 Million cell updates/sec

Title: US-10-728-051-1
Perfect score: 2032
Sequence: 1 aataatcatatattcattc.....cggttgcggtgtttcttc 2032

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_est7:*

7: gb_est8:*

8: gb_est9:*

9: gb_est10:*

10: gb_est11:*

11: gb_est12:*

12: gb_est13:*

13: gb_est14:*

14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	719	35.4	721	4	CD038628
2	713	35.1	714	4	CD038277
3	711.4	35.0	723	4	CD038527
4	681	33.5	717	4	CD038837
5	657.2	32.3	724	4	CD038648
6	629.2	31.0	719	4	CD038172
7	626	30.8	676	4	CD038790
8	602	29.6	685	4	CD038555
9	576	28.3	588	4	CD038119
10	527.6	26.0	684	4	CD038540
11	473	23.3	474	4	CD038694
12	471	23.2	582	4	CD038620
13	458.8	22.6	509	4	CD038253
14	436	21.5	484	4	CD038101
15	428.6	21.1	443	8	CO897502
16	425	20.9	425	4	CD038284
17	419.6	20.6	536	4	CD038075
18	392	19.3	411	8	CO897503
19	358.6	17.6	406	4	CD038765

20	307.6	15.1	823	4	CA858229	CA858229	EST635484
21	306.2	15.1	851	4	CA858769	CA858769	EST636024
22	296.8	14.6	894	4	CA858664	CA858664	EST635919
23	296.6	14.6	806	2	BI310422	BI310422	EST531217
24	292.2	14.4	864	3	BI312471	BI312471	EST609047
25	290.8	14.3	780	2	BI311149	BI311149	EST531289
26	290.6	14.3	823	3	BI312251	BI312251	EST608090
27	290	14.3	862	3	BI312313	BI312313	EST608807
28	285.8	14.1	854	3	BI312341	BI312341	EST608987
29	285.4	14.0	830	4	CA858151	CA858151	EST635406
30	283	13.9	805	2	BI312339	BI312339	EST531408
31	281.4	13.8	760	4	CA858137	CA858137	EST635392
32	281.4	13.8	769	2	BI311022	BI311022	EST531277
33	280.2	13.8	847	4	CA858293	CA858293	EST635548
34	278.4	13.7	781	2	BI311613	BI311613	EST531336
35	274.6	13.5	765	3	BI312251	BI312251	EST608086
36	273.2	13.4	804	4	CA858167	CA858167	EST635422
37	272.4	13.4	843	2	BI311012	BI311012	EST531276
38	271.8	13.4	805	4	CA858433	CA858433	EST635688
39	271.4	13.4	734	4	CA858790	CA858790	EST636045
40	271.4	13.4	839	2	BI311235	BI311235	EST531298
41	271.2	13.3	861	4	CA858864	CA858864	EST636119
42	271	13.3	860	3	BI312453	BI312453	EST608029
43	270.4	13.3	701	3	BI312484	BI312484	EST610416
44	270.4	13.3	727	2	BI309850	BI309850	EST531160
45	270.4	13.3	837	2	BI310945	BI310945	EST531269

ALIGNMENTS

RESULT 1
LOCUS CD038628 721 bp mRNA linear EST 07-MAY-2003
DEFINITION UTPPI010_A05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI010_A05 5', mRNA sequence.

ACCESSION CD038628
VERSION CD038628.1 GI:30420466
KEYWORDS EST.

SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea

REFERENCE 1 (bases 1 to 721)
AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
TITLE Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL Unpublished (2003)
COMMENT Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3

FEATURES
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/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI010_A05"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/notes="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV1XAR4). A13 has resistance to Aspergillus infection"

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 35.4%; Score 719; DB 4; Length 721;
Best Local Similarity 99.7%; Pred. No. 6.3e-191;
Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1231 CACCAACCCCAATCAACTTGAGAGAGCGGAGCCGATCTTTCTAAACAACCTTTGGGAAGTT 1290
Db 1 CACCAACCCCAATCAACTTGAGAGAGCGGAGCCGATCTTTCTAAACAACCTTTGGGAAGTT 60

Qy 1291 ATTTGAGGTGAAGCCGACAGAAGAACCCGCCAGCTTCAGGACCTGGACATGATGCTCAC 1350
Db 61 ATTTGAGGTGAAGCCGACAGAAGAACCCGCCAGCTTCAGGACCTGGACATGATGCTCAC 120

Qy 1351 CTGTGTAGATCAAGAAGAGGACTTTGATGCTCCACACTTCAACTCAAGGCCATGTT 1410
Db 121 CTGTGTAGATCAAGAAGAGGACTTTGATGCTCCACACTTCAACTCAAGGCCATGTT 180

Qy 1411 TATCGTCGTCGTCACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAGAAAAGAGCA 1470
Db 181 TATCGTCGTCGTCACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGTAGAAAAGAGCA 240

Qy 1471 ACACAGAGGGGCGCGGGAAGAAGAGGAGGACGAAGACGAAGAAGAGGAGGGAAGTAA 1530
Db 241 ACACAGAGGGGCGCGGGAAGAAGAGGAGGAGGACGAAGACGAAGAAGAGGAGGGAAGTAA 300

Qy 1531 CAGAGAGTCCGTAGGTACACAGGAGTTGAAGGAAGGGATGTTCTATCATGCCAGC 1590
Db 301 CAGAGAGTCCGTAGGTACACAGGAGTTGAAGGAAGGGATGTTCTATCATGCCAGC 360

Qy 1591 AGCTCATCCAGTAGCCATCAACGCTTCTCCGAACCTCCATCTGCTTGGCTTCGGTATCAA 1650
Db 361 AGCTCATCCAGTAGCCATCAACGCTTCTCCGAACCTCCATCTGCTTGGCTTCGGTATCAA 420

Qy 1651 CGCTGAAAACAACACAGAAATCTTCTTGCAGGTGATAAGGACAATGTGTATAGACCAGAT 1710
Db 421 CGCTGAAAACAACACAGAAATCTTCTTGCAGGTGATAAGGACAATGTGTATAGACCAGAT 480

Qy 1711 AGAGAGCAAGCAAGATTTAGATTCCTCGGTGGGTGAACAAGTTGAGAAGTCTCAT 1770
Db 481 AGAGAGCAAGCAAGATTTAGATTCCTCGGTGGGTGAACAAGTTGAGAAGTCTCAT 540

Qy 1771 CAAAAACCAAGGAATCTCACATTTGTGAGTGTCTGCTCCATCTCAATCTCAATCTCC 1830
Db 541 CAAAAACCAAGGAATCTCACATTTGTGAGTGTCTGCTCCATCTCAATCTCAATCTCC 600

Qy 1831 GTCGTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAAAACCAAGAGG 1890
Db 601 GTCGTCTCTGAGAAAGAGTCTCTGAGAAAGAGGATCAAGAGGAGGAAAAACCAAGAGG 660

Qy 1891 GAGGGTCCACTCTTTCAATTTGAGGCTTTTAACTGAGATGAGGCAACTTGTAT 1950
Db 661 GAGGGTCCACTCTTTCAATTTGAGGCTTTTAACTGAGATGAGGCAACTTGTAT 720

Qy 1951 G 1951
Db 721 G 721

RESULT 2
CD038277

LOCUS
DEFINITION

CD038277 714 bp mRNA linear EST 07-MAY-2003
Arachis hypogaea cDNA clone UTPPI005_A03 5', mRNA sequence.
CD038277
EST.
CD038277.1 GI:30420115

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 714)
Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.

FEATURES
source

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/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI005_A03"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="Xhl-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCV11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 35.1%; Score 713; DB 4; Length 714;
Best Local Similarity 99.9%; Pred. No. 3.1e-189;
Matches 713; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 146 ABAACAGAGAACCCCTGCGCCAGAGGTGCTCCAGAGTTGTCAACAGGAAACCGATGAC 205
Db 1 ABAACAGAGAACCCCTGCGCCAGAGGTGCTCCAGAGTTGTCAACAGGAAACCGATGAC 60

Qy 206 TTGAAGCAAAAGGCATCGGAGTCTCGTCGACCAAGCTCGAGTATGATCTCGTTGTGTC 265
Db 61 TTGAAGCAAAAGGCATCGGAGTCTCGTCGACCAAGCTCGAGTATGATCTCGTTGTGTC 120

Fax: 229-387-2321
Email: bguo@tifon.usda.gov
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..724
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI010.C11"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XLI-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat bang."

Query Match 32.3%; Score 657.2; DB 4; Length 724;
Best Local Similarity 95.9%; Pred. No. 1.8e-173;
Matches 697; Conservative 0; Mismatches 24; Indels 6; Gaps 2;

QY 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCACCTCAGATCCAGATCCCATCCGTTT 858
DB 1 CAATAACAGAAAGAGCTTTAATCTTGACGAGGGCCATGCACCTCAGATCCCATCCGTTT 60
QY 859 CATTTCTACATCTTGAAACCGCCATGACCAACCACTCAGAGTAGCTAAATCTCCAT 918
DB 61 CATTTCTACATCTTGAAACCGCCATGACCAACCACTCAGAGTAGCTAAATCTCCAT 120
QY 919 GCCCGTTAACACACCCCGCCAGTTTGAGGATTTCTTCCCGCGAGCCGAGACCAATC 978
DB 121 GCCCGTTAACACACCCCGCCAGTTTGAGGATTTCTTCCCGCGAGCCGAGACCAATC 180
QY 979 ATCTACTTCGAGGCTTCACGAGGATACGTTGGAGGCGCCTTCAATCGGATTCAA 1038
DB 181 ATCTACTTCGAGGATTCACGAGGATACGTTGGAGGCGCCTTCAATCGGATTCAA 240
QY 1039 TGAGATACGAGGGTGTCTGTAGAAAGAGATGACGAGAGTGAGCAAGAGGAGAGGGCA 1098
DB 241 TGAGATACGAGGGTGTCTGTAGAAAGAGATGACGAGAGTGAGCAAGAGGAGAGGGCA 300
QY 1099 GAGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGATAGTCAAGTGTCAA 1158
DB 301 GAGCGAGCGGAGTACTCGGAGTAGTG--ATAATGAAGGAGTGATAGTCAAGTGTCAA 357
QY 1159 GGACACGTTGAAGAACTTACTAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAGA 1218
DB 358 GGACACGTTGAAGAACTTACTAGCAGCGTAAATCGTCTCAAGAAAGGCTCC--GA 414
QY 1219 AGAGGAGATATACCAACCAATCAACTTGAGAGAGGCGAGCCGATCTTTCTAAACAA 1278
DB 415 AGAGGAGATATACCAACCAATCAACTTGAGAGATGGGAGGCCCGATCTTTCTAAACAA 474
QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAGAACCCCGAGCTTCAGGACCTGGA 1338

Db 475 CTTTGGGAGGTATTATTGAGGTGAAGCCAGACAAGAAACCCCGAGCTTCAGGACCTGGA 534
QY 1339 CATGATGCTCACCTGCTAGAGATCAAGAGGAGCTTTGATGCTCCACACATTCAACTC 1398
Db 535 CATGATGCTCACCTGCTAGAGATCAAGAGGAGCTTTGATGCTCCACACATTCAACTC 594
QY 1399 AAAGGCCATGTTATCTGCTCGTCAACAAAGGAACCTTGAACCTCGTGGCTGT 1458
Db 595 AAAGGCCATGTTATCTGCTCGTCAACAAAGGAACCTTGAACCTCGTGGCTGT 654
QY 1459 AAGAAAAGAGCAACACAGAGGGGACGCGGGGAAGAGAGGAGCAAGACGAGGAAGA 1518
Db 655 AAGAAAAGAGCAACACAGAGGGGACGCGGGGAAGAGAGTGGGAAGAGGAGGAAGA 714
QY 1519 GGAGGGA 1525
Db 715 TGAAGAA 721

RESULT 6
CD038172
LOCUS
DEFINITION
CD038172
ACCESSION
CD038172
VERSION
CD038172.1
KEYWORDS
EST.
SOURCE
Arachis hypogaea (peanut)
ORGANISM
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.
REFERENCE
1 (bases 1 to 719)
Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G. and Lynch, R. E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
JOURNAL
COMMENT
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifon.usda.gov
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..719
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI003_D10"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XLI-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into

Db 241 GAGGTGAGCAAGAGGAGAGGCGGAGGCGGATCGAGTACTCGAGTAGTGAGAACAAATG 300
 QY 1134 AAGGAGTGATAGTCAAAAGTGTCAAAGGAGCAGCTGTGAAGAACTTACTAAGCACGCTAAAT 1193
 Db 301 AAGGAGTGATAGTCAAAAGTGTCAAAGGAGCAGCTGTGAAGAACTTACTAAGCACGCTAAAT 360
 QY 1194 CCGTCTCAAAGAAAGGCTCCGAGAGAGGAGGAGATACCAACCCCAATCAACTTGGAG 1253
 Db 361 CCGTCTCAAAGAAAGGCTCCGAGAGAGGAGGAGATACCAACCCCAATCAACTTGGAG 420
 QY 1254 AAGGAGGCGCGATCTTCTTAACAACCTTGGAGGTTATTTGAGTGAAGCCAGACAG- 1312
 Db 421 AAGCGAGCGCGATCTTCTTAACAACCTTGGAGGTTATTTGAGTGAAGCCAGACNAGN 480
 QY 1313 AAGAACCCCGGAGCTTCAGGACCTGGACATGATGCTCA-CTGTGTAGAGATCAAGAAGG 1371
 Db 481 AAGAACCCCGGAGCTTCAGGACCTGGACATGATGCTCACTGCTGATAGATCAAGAAGG 540
 QY 1372 AGCTTTGATGCTCCACACTTCAACTCAAAGGCGATGTTATCGTCTGCTCAACAAGG 1431
 Db 541 AGCTTTGATGCTCCACACTTCAACTCAAAGGCGATGTTATCGTCTGCTCAACAAGG 600
 QY 1432 AACTGGAAACCTTGAACCTGCTGGCTGTAAAGAAAGACCAACAGAGGGGACGGCGG- 1490
 Db 601 AACTGGAAACCTTGAACCTGCTGGCTGT-AGAAAAGAGCAACAACNGAGGGGACGGCGG 659
 QY 1491 AAGAAGAGGAGGAGCGAA 1507
 Db 660 AAGAGAGGAGGAGCGAA 676

RESULT 8

CD038555
 LOCUS
 DEFINITION UTPPI009_A05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
 Arachis hypogaea cDNA clone UTPPI009_A05 5', mRNA sequence.

ACCESSION CD038555

VERSION CD038555.1

KEYWORDS G1:30420393

SOURCE EST.

ORGANISM Arachis hypogaea (peanut)

Arachis hypogaea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
 Aeschynomeneae; Arachis.

1 (bases 1 to 685)

REFERENCE Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.

AUTHORS and Lynch,R.E.

TITLE Generation and Analyses of ESTs for Arachis hypogaea

JOURNAL Unpublished (2003)

COMMENT Contact: Baozhu Guo

Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit

2747 Davis Rd., Tifton, GA 31794, USA

Tel: 229-387-2334

Fax: 229-387-2321

Email: bguo@tifton.usda.gov

Seq primer: T3

FEATURES Location/Qualifiers

source

1..685

/organism="Arachis hypogaea"

/mol_type="mRNA"

/cultivar="A13"

/db_xref="taxon:3818"

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/tissue_type="Immature pods"

/dev_stage="R6"

/lab_host="Xl1-blue"

/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library

(UTPP)"

/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;

cDNA library was constructed from peanut cultivar A13

(NCV11XAR4). A13 has resistance to Aspergillus infection

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapur (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat dang."

ORIGIN

Query Match 29.6%; Score 602; DB 4; Length 685;
 Best Local Similarity 94.3%; Pred. No. 6.6e-158;
 Matches 663; Conservative 0; Mismatches 21; Indels 19; Gaps 3;
 QY 29 ATATAGTAGTAGCAGAGCAATGAGAGGAGGGTTTCTCCACTGATGCTGTGCTAGGG 88
 Db 1 ATATAAGTAGTTGACGAGCAATGAGAGGAGGGTTTCTCCACTGATGCTGTGCTAGGG 60
 QY 89 ATCTTTGCTCTGGCTTCAGTTTCTGCAACGCGATGCCAAGTCATCACCTTACCGAAGAAA 148
 Db 61 ATCTTTGCTCTGGCTTCAGTTTCTGCAACGCGAGCCCAAGTCACC-----TTACCGAAGAAA 114
 QY 149 ACAGAGAAACCCCTGCGCCAGAGGTGCTCCAGAGTTGTCAACAGGAACCGGATGACTTG 208
 Db 115 ACAGAGAAACCCCTGCGCCAGAGGTGCTCCAGAGTTGTCAACAGGAACCGGAGACTTG 174
 QY 209 AAGCAAAAGCGATGCGAGTCTCGTCGACCAAGCTCGAGTATGATCTCTGTTGTTCTAT 268
 Db 175 AAGCAAAAGCGATGCGAGTCTCGTCGACCAAGCTCGAGTATGATCTCTGTTGTTCTAT 234
 QY 269 GATCCTCGAGGACACACTGGCACCAACCAACGTTTCCCTCCAGGGGAGCGGACACGT 328
 Db 235 G-----ACACTGGCGCCACCAACCAAGTCACCTCCAGGGGAGCGGACACGT 282
 QY 329 GGCCGCCAACCCCGAGACTACGATGATGACCGCGCTCAACCCCGAAGAGAGGAGGAGGC 388
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RESULT 9

CD038119

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LOCUS       CD038119               588 bp      mRNA      linear      EST 07-MAY-2003
DEFINITION   UTPI002_F11 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
ACCESSION   CD038119
VERSION     CD038119.1 GI:30419957
KEYWORDS    EST.
SOURCE      Arachis hypogaea (peanut)
ORGANISM    Arachis hypogaea
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
             rosids; eutrosids I; Fabales; Fabaceae; Papilionoideae;
             Aeschynomeneae; Arachis.
REFERENCE   1 (bases 1 to 588)
AUTHORS     Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
             and Lynch,R.E.
TITLE       Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL     Unpublished (2003)
COMMENT     Contact: Baozhu Guo
             Molecular Genetics
             USDA/ARS, Crop Protection and Management Research Unit
             2747 Davis Rd., Tifton, GA 31794, USA
             Tel: 229-387-2334
             Fax: 229-387-2321
             Email: bguo@tifton.usda.gov
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                 (UTPP)"
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                 cDNA library was constructed from peanut cultivar A13
                 (NCV11X44). A13 has resistance to Aspergillus infection
                 and drought tolerance. The immature pods that developed to
                 R6 stage were collected from different plants, and placed
                 into liquid N2 immediately and stored in -80oC freezer.
                 Total RNA was isolated with TRIzol-Reagent
                 ultrapur (GIBCOBRL). mRNA was extracted and purified from
                 total RNA (Promega). cDNA synthesis and library
                 construction followed the protocol of by ZAP-cDNA Gigapack
                 III Gold cloning kit (Stratagene). The cDNA above 500bp
                 were collected after size-fraction. The inserts were
                 directionally cloned into Uni-ZAP XR vector using XhoI
                 EcoRI sites adapters. The lambda library was packed into
                 phages using Gigapack III Gold (Stratagene). The
                 un-amplified library was used to excise pBluescript
                 phagemids from the Uni-ZAP XR vector, and the phagemids
                 was used to transform the host bacteria SOLR. The library
                 was constructed by Dr. Meng Luo and Dr. Phat Dang."
ORIGIN
Query Match      28.3%; Score 576; DB 4; Length 588;
Best Local Similarity 99.8%; Pred. No. 1.4e-150;
Matches 587; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY      1558  GTTGAAGGAAGGCGATGTGTTTCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTC 1617
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QY      1917  AGGCTTTTAACTGAGAAATGGAGCAACTTGTATTATGATATGATATGATATGATATGATATGAT 1976
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QY      1977  TACTCTACTACTCCAAAAACTTATCAATAAATAAAAAAGTTTGTGCGTT 2024
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ACCESSION CD038540
VERSION     CD038540.1 GI:30420378
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ORGANISM    Arachis hypogaea
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             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
             rosids; eutrosids I; Fabales; Fabaceae; Papilionoideae;
             Aeschynomeneae; Arachis.
REFERENCE   1 (bases 1 to 684)
AUTHORS     Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
             and Lynch,R.E.
TITLE       Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL     Unpublished (2003)
COMMENT     Contact: Baozhu Guo
             Molecular Genetics
             USDA/ARS, Crop Protection and Management Research Unit
             2747 Davis Rd., Tifton, GA 31794, USA
             Tel: 229-387-2334
             Fax: 229-387-2321
             Email: bguo@tifton.usda.gov
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                 /notes="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
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                 and drought tolerance. The immature pods that developed to
                 R6 stage were collected from different plants, and placed
                 into liquid N2 immediately and stored in -80oC freezer.
                 Total RNA was isolated with TRIzol-Reagent
                 ultrapur (GIBCOBRL). mRNA was extracted and purified from
                 total RNA (Promega). cDNA synthesis and library
                 construction followed the protocol of by ZAP-cDNA Gigapack
                 III Gold cloning kit (Stratagene). The cDNA above 500bp
                 were collected after size-fraction. The inserts were
                 directionally cloned into Uni-ZAP XR vector using XhoI
                 EcoRI sites adapters. The lambda library was packed into
                 phages using Gigapack III Gold (Stratagene). The
                 un-amplified library was used to excise pBluescript
                 phagemids from the Uni-ZAP XR vector, and the phagemids
                 was used to transform the host bacteria SOLR. The library
                 was constructed by Dr. Meng Luo and Dr. Phat Dang."

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1745 TCGGGTGAAACAAGTTGAGAGCTCATCAAAACACAGAGGAATCTCACCTTTGTGAGTGCT 1804
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1805 CGTCTCAATCTCAATCTCAATCTCGCTCGCTCTCTCTGAGAAAGAGTCTCTGAGAAAGAG 1864
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RESULT 15

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LOCUS EST00007 Peanut Lambda Express library Arachis hypogaea cDNA 5',
DEFINITION mRNA sequence.

ACCESSION CO897502
VERSION CO897502.1 GI:51237292
KEYWORDS EST.
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Yan, Y.S., Wang, L., Zhong, Y.J. and Huang, S.Z.
TITLE Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL Unpublished (2004)
COMMENT Contact: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
Guangzhou, 510275, China
Tel: (860) 02084036592
Email: yys9803@yahoo.com.cn
Seq primer: pTriplex2 Forward.

FEATURES
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GenCore version 5.1.9
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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

US-09-106-872A-21

; Sequence 21, Application US/09106872A

; Patent No. 6486311

; GENERAL INFORMATION:

; APPLICANT: Burks Jr., A. Wesley

; APPLICANT: Stanley, J. Steven

; APPLICANT: Cockrell, Gael

; APPLICANT: King, Nina E.

; APPLICANT: Sampson, Hugh A.

; APPLICANT: Helm, Ricki M.

; APPLICANT: Bannon, Gary A.

; TITLE OF INVENTION: Peanut Allergens and Methods

; FILE REFERENCE: HS 103 CIP

; CURRENT APPLICATION NUMBER: US/09/106, 872A

; PRIOR APPLICATION DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: PCT/US96/15222

; PRIOR FILING DATE: 1996-09-23

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 2032

; TYPE: DNA

; ORGANISM: Atachis hypogaea

US-09-106-872A-21

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DB 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGCTCGCTCGTGAAGAGAGTCTCCTCAGAA 1860
QY 1861 AGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
DB 1861 AGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
QY 1921 TTTTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980
DB 1921 TTTTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1980
QY 1981 CTACTATCCAAAACCTTATCAATAATAAAGGTTTGTGCGTTGTTCTCC 2032
DB 1981 CTACTATCCAAAACCTTATCAATAATAAAGGTTTGTGCGTTGTTCTCC 2032

RESULT 2

US-09-191-593-5
; Sequence 5, Application US/09191593
; Patent No. 6835824
; GENERAL INFORMATION:
; APPLICANT: BURKS, A Wesley, HELM, Ricki M,
; APPLICANT: COCKRELL, Gael, STANLEY, J Steven,
; APPLICANT: BANNON, Gary A
; TITLE OF INVENTION: PEANUT ALLERGENS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Head, Johnson & Kachigian
; STREET: 112 W. Center St., Suite 230
; CITY: Fayetteville
; STATE: Arkansas AR
; COUNTRY: United States of America
; ZIP: 72701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Wordperfect 6.0C
; CURRENT APPLICATION DATA:


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1021 CTTCAATCGGAATTCATAGATACGAGGGTCTGTAGAGAAATCGAGAGTGA 1080
QY 1081 GCAAGAGGAGAGGCGAGAGGCGATCGAGTACTCGAGTAGTGAACAATCAAGGAGT 1140
Db 1081 GCAAGAGGAGAGGCGAGAGGCGATCGAGTACTCGAGTAGTGAACAATCAAGGAGT 1140
QY 1141 GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTC 1200
Db 1141 GATAGTCAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTC 1200
QY 1201 AAGAAGGCTCCGAAGAGGAGGAGATATCAACCAACCCCAATCACTTGAGAGAAGCGGA 1260
Db 1201 AAGAAGGCTCCGAAGAGGAGGAGATATCAACCAACCCCAATCACTTGAGAGAAGCGGA 1260
QY 1261 GCCCGATCTTTCTAAACAACCTTTGGGAAGTTATTGAGGTGAAGCCAGACAAGAGAACC 1320
Db 1261 GCCCGATCTTTCTAAACAACCTTTGGGAAGTTATTGAGGTGAAGCCAGACAAGAGAACC 1320
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Db 1321 CAGCTTCAGGACCTGGACATGATGCTACCTGTGTAGAGATCAAGAAGGAGCTTTGAT 1380
QY 1381 GCTCCACACTTCAACTCAAAAGGCCATGGTTATCGTCGTCAACAAGGAACCTGAAA 1440
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QY 1441 CTTGAACTCGTGGCTTGAAGAAAGAGCAACAACAGAGGGGACGGCGGAAGAGGA 1500
Db 1441 CTTGAACTCGTGGCTTGAAGAAAGAGCAACAACAGAGGGGACGGCGGAAGAGGA 1500
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Db 1501 GGAAGAGCAAGAGAGGAGGGAAGTAAACAGAGAGTGCCTAGGTACACAGCGAGGTT 1560
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Db 1561 GAAGGAAGGCGATGTGTTCATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTC 1620
QY 1621 CGAACTCCATCTCGCTTGGCTTCGGTATCAACGCTGAAACCAACCAAGAACTTCTCTTC 1680
Db 1621 CGAACTCCATCTCGCTTGGCTTCGGTATCAACGCTGAAACCAACCAAGAACTTCTCTTC 1680
QY 1681 AGTGATAGGACAATGTGATAGACCATAGAGAGCAAGCAAGGATTTAGCATTCCTC 1740
Db 1681 AGTGATAGGACAATGTGATAGACCATAGAGAGCAAGCAAGGATTTAGCATTCCTC 1740
QY 1741 TGGGTCGGGTGAACAAGTTGAGAGCTCATCAAAAACCAAGAGAACTCTCACTTTGTAG 1800
Db 1741 TGGGTCGGGTGAACAAGTTGAGAGCTCATCAAAAACCAAGAGAACTCTCACTTTGTAG 1800
QY 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCGTCTCGTGAAGAGAGTCTCCTGAGAA 1860
Db 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCGTCTCGTGAAGAGAGTCTCCTGAGAA 1860
QY 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGCTCCACTCTTCAATTTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGGAGGAAACCAAGAGGAGGAGGCTCCACTCTTCAATTTTGAAGGC 1920
QY 1921 TTTTAACTGAGAAATGGAGGCAACTTGTATGTATCGATATAAGATCAAGCTTTTGTACT 1980
Db 1921 TTTTAACTGAGAAATGGAGGCAACTTGTATGTATCGATATAAGATCAAGCTTTTGTACT 1980
QY 1981 CTACTATCCAAAACCTTATCAATAAATAAAGCTTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCCAAAACCTTATCAATAAATAAAGCTTTGTGCGTTGTTCTCC 2032
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RESULT 3
US-09-715-036-5
; Sequence 5, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:

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; APPLICANT: DODO, HORTENSE W.  
; APPLICANT: ARNTZEN, CHARLES J.  
; APPLICANT: KONAN, KOFFI N'DA  
; APPLICANT: VIQUEZ, OLGA  
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN  
; FILE REFERENCE: 072121/0104  
; CURRENT APPLICATION NUMBER: US/09/715,036  
; CURRENT FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: 60/167,255  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 2032  
; TYPE: DNA  
; ORGANISM: Arachis hypogaea  
US-09-715-036-5
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Query Match 100.0%; Score 2032; DB 3; Length 2032;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60  
Db 1 AATAATCATATATATTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60  
QY 61 GGTTCCTCCACTGATCTGTGCTAGGGATCCTTTGCTGGCTTCAGTTTCTGCAACGCA 120  
Db 61 GGTTCCTCCACTGATCTGTGCTAGGGATCCTTTGCTGGCTTCAGTTTCTGCAACGCA 120  
QY 121 TGCCAAGTCTACCTTACAGAGAAAAACAGAGAAACCCCTGCGCCAGAGGTCCTCCA 180  
Db 121 TGCCAAGTCTACCTTACAGAGAAAAACAGAGAAACCCCTGCGCCAGAGGTCCTCCA 180  
QY 181 GAGTTCTCAACAGGAACCGGATGACTTGAAGCAAAAGGATGCGAGTCTCGCTGCACCA 240  
Db 181 GAGTTCTCAACAGGAACCGGATGACTTGAAGCAAAAGGATGCGAGTCTCGCTGCACCA 240  
QY 241 GCTCGAGTATGATCTCTGTTGTCTATGATCTCGAGGACACATGGGACCAACCAACCA 300  
Db 241 GCTCGAGTATGATCTCTGTTGTCTATGATCTCGAGGACACATGGGACCAACCAACCA 300  
QY 301 AGTTCCCTCCAGGGGAGCGGACACGTCGCCCAACCGGAGACTACGATGATGACCG 360  
Db 301 AGTTCCCTCCAGGGGAGCGGACACGTCGCCCAACCGGAGACTACGATGATGACCG 360  
QY 361 CGGTCAACCCCGAAGAGAGAGGAGCGGATGGGACCGAGCTGGACCGAGGGAGCGTGA 420  
Db 361 CGGTCAACCCCGAAGAGAGAGGAGCGGATGGGACCGAGCTGGACCGAGGGAGCGTGA 420  
QY 421 AGAGAAAGAGACTTGAGACCAACAGAGAGAGATTGGAGCGACCAAGTCTCAGCAGCC 480  
Db 421 AGAGAAAGAGACTTGAGACCAACAGAGAGAGATTGGAGCGCGCAAGTCTCAGCAGCC 480  
QY 481 ACGGAAATAAGGCCCGAAGGAGAGAGAGAAAGAGAGTGGGGAACACACAGGTAGCCA 540  
Db 481 ACGGAAATAAGGCCCGAAGGAGAGAGAGAGAAAGAGTGGGGAACACACAGGTAGCCA 540  
QY 541 TGTGAGGAGAAACAATCTCGGAACAACCTTTCTACTTTCCCTCAAGCGGTTTAGCAC 600  
Db 541 TGTGAGGAGAAACAATCTCGGAACAACCTTTCTACTTTCCCTCAAGCGGTTTAGCAC 600  
QY 601 CCGCTACGGGAACCAAAACCGTAGGATCGGGTCTTCAGAGGTTTGAACCAAGGTCAG 660  
Db 601 CCGCTACGGGAACCAAAACCGTAGGATCGGGTCTTCAGAGGTTTGAACCAAGGTCAG 660  
QY 661 GCAGTTTCAGAACTCTCCAGAACTCACCGTATTGTGCAGATCGAGGCCAAACTAACCTCT 720  
Db 661 GCAGTTTCAGAACTCTCCAGAACTCACCGTATTGTGCAGATCGAGGCCAAACTAACCTCT 720  
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Db 721 TGTTCCTCCCAAGCAGCGTGATGCTGATAATCATCTTTGTTATCCAGAGGGCAGCCAC 780
Qy 781 CGTGACCGTAGCAATGCGCAATAACAGAAAGAGCTTTAATCTTGCAGGCGCATGCACT 840
Db 781 CGTGACCGTAGCAATGCGCAATAACAGAAAGAGCTTTAATCTTGCAGAGGCGCATGCACT 840
Qy 841 CAGAAATCCCAATCCGGTTTCAATTTCCCTACATCTTGAACCGGCATGACAAACAGAACTCTCAG 900
Db 841 CAGAAATCCCAATCCGGTTTCAATTTCCCTACATCTTGAACCGGCATGACAAACAGAACTCTCAG 900
Qy 901 AGTAGCTTAAATCTCCATGCCGTTTACACACCCGGCCAGTTTGAAGATTTCTTCCCGGC 960
Db 901 AGTAGCTTAAATCTCCATGCCGTTTAAACACCCGGCCAGTTTGAAGATTTCTTCCCGGC 960
Qy 961 GAGCAGCGGAGACCAATCATCTTACTTGCAGGGCTTCAGCAGGAATACTGTTGAGGCGGC 1020
Db 961 GAGCAGCGGAGACCAATCATCTTACTTGCAGGGCTTCAGCAGGAATACTGTTGAGGCGGC 1020
Qy 1021 CTTCAATGCGGAATTCATGAGATACGAGGGTCTGTTAGAGAGAAATGAGAGGTGA 1080
Db 1021 CTTCAATGCGGAATTCATGAGATACGAGGGTCTGTTAGAGAGAAATGAGAGGTGA 1080
Qy 1081 GCAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTCAGAACAAATGAGGAGT 1140
Db 1081 GCAGAGGAGAGGGCAGAGGCGATGAGTACTCGGAGTAGTCAGAACAAATGAGGAGT 1140
Qy 1141 GATAGTCAAAAGTGTCAAGAGCAGCTTTGAAGAACTTACTAAGCAGCGTAAATCCGTC 1200
Db 1141 GATAGTCAAAAGTGTCAAGAGCAGCTTTGAAGAACTTACTAAGCAGCGTAAATCCGTC 1200
Qy 1201 AAGAAAGGCTCCGAGAGAGAGGAGATATCAACAAACCAATCAACTTTGAGAGAGCGA 1260
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Qy 1261 GCCGATCTTTCTTAAACAACTTTGGGAGTTATTTGAGGTGAAGCAAGCAAGAACCC 1320
Db 1261 GCCGATCTTTCTTAAACAACTTTGGGAGTTATTTGAGGTGAAGCAAGCAAGAACCC 1320
Qy 1321 CCAGCTTCAGGACCTGGACATGATGCTCAGCTGTGAGAGATCAAGAGAGGCTTTGAT 1380
Db 1321 CCAGCTTCAGGACCTGGACATGATGCTCAGCTGTGAGAGATCAAGAGAGGCTTTGAT 1380
Qy 1381 GTCCCAACACTTCAACTCAAGGCCATGTTATGCTGCTGCTCAACAAAGGAACTGGAA 1440
Db 1381 GTCCCAACACTTCAACTCAAGGCCATGTTATGCTGCTGCTCAACAAAGGAACTGGAA 1440
Qy 1441 CTTTGAACCTGCTGTAGAAAGCAACACAGAGGGGCGCGGGAAGAGGA 1500
Db 1441 CTTTGAACCTGCTGTAGAAAGCAACACAGAGGGGCGCGGGAAGAGGA 1500
Qy 1501 GGACGAAGACGAAGAGAGGGGAAAGTAAACAGAGAGGTGCGGTAGGTACACAGCGAGTT 1560
Db 1501 GGACGAAGACGAAGAGAGGGGAAAGTAAACAGAGAGGTGCGGTAGGTACACAGCGAGTT 1560
Qy 1561 GAAGAGGCGATGTTGTTATCATGTCAGAGCTCATTCAGTAGCCATCAACGCTTCTC 1620
Db 1561 GAAGAGGCGATGTTGTTATCATGTCAGAGCTCATTCAGTAGCCATCAACGCTTCTC 1620
Qy 1621 CGAACTCCATCTCTGCTTGGCTTCGGTATCAACGCTGAAACCAACAGATCTTCTTGC 1680
Db 1621 CGAACTCCATCTCTGCTTGGCTTCGGTATCAACGCTGAAACCAACAGATCTTCTTGC 1680
Qy 1681 AGGTGATAGGACAAATGTGTAGACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740
Db 1681 AGGTGATAGGACAAATGTGTAGACAGATAGAGAGCAAGCGAAGATTTAGCATTTCC 1740
Qy 1741 TGGGTGCGGTGAACAAAGTTGAGAGGCTCATCAAAAAACAGAGGAATCTCATTTGTGAG 1800
Db 1741 TGGGTGCGGTGAACAAAGTTGAGAGGCTCATCAAAAAACAGAGGAATCTCATTTGTGAG 1800
Qy 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTGAGAA 1860
Db 1801 TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTGAGAA 1860

Qy 1861 AGAGGATCAAGAGAGGAAAAACAAGGAGGAGGTCCTCTCTTCAATTTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGAGGAAAAACAAGGAGGAGGTCCTCTCTTCAATTTTGAAGGC 1920
Qy 1921 TTTTAACTGAGAATGAGAGCAACTTGTATGATATGATAAATAGATCACGCTTTGTACT 1980
Db 1921 TTTTAACTGAGAATGAGAGCAACTTGTATGATATGATAAATAGATCACGCTTTGTACT 1980
Qy 1981 CTACTATCCAAAACTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC 2032
Db 1981 CTACTATCCAAAACTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC 2032

RESULT 4

US-09-106-872A-23
; Sequence 23, Application US/09106872A
; Patent No. 6486311
; GENERAL INFORMATION:
; APPLICANT: Burks Jr., A. Wesley
; APPLICANT: Stanley, J. Steven
; APPLICANT: Cockrell, Gael
; APPLICANT: King, Nina E.
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Helm, Ricki M.
; APPLICANT: Bannon, Gary A.
; TITLE OF INVENTION: Peanut Allergens and Methods
; FILE REFERENCE: HS 103 CIP
; CURRENT APPLICATION NUMBER: US/09/106, 872A
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: PCT/US96/15222
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-09-106-872A-23

Query Match 100.0%; Score 2032; DB 3; Length 2041;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATAATCATATATATTTTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60
Db 1 AATAATCATATATTTTCATCAATCATCTATATAAGTAGTAGCAGGAGCAATGAGAGGAG 60
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Db 61 GGTTCCTCCACTGATGCTGTGCTAGGGATCTCTTGTCTGCTGCTTCTAGTTTCTGCAACGCA 120
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Db 121 TGCCAAGTATCATCTTACAGNAGAAACAGAGAACCCCTGCGCCAGAGGTCCTTCCA 180
Qy 181 GAGTTGCTCAACAGGAACCGGATGACTTGAAGCAAAAAGGATGCGAGTCTCGCTGCACAA 240
Db 181 GAGTTGCTCAACAGGAACCGGATGACTTGAAGCAAAAAGGATGCGAGTCTCGCTGCACAA 240
Qy 241 GCTCGAGTATGATCTCTGTTGTGTCTATGATCTCTCGAGGACACATGCGGACCAACCA 300
Db 241 GCTCGAGTATGATCTCTGTTGTGTCTATGATCTCTCGAGGACACATGCGGACCAACCA 300
Qy 301 AGTTTCCCTCCAGGGGAGGAGCAGCTGCGCCCAACCCGGAGACTACGATGATGACCG 360
Db 301 AGTTTCCCTCCAGGGGAGGAGCAGCTGCGCCCAACCCGGAGACTACGATGATGACCG 360
Qy 361 CCGTCAACCCCGAAGAGAGAGGAGCGATGGGACCAAGCTGGACCCAGCTGGACCGGAGGTGA 420
Db 361 CCGTCAACCCCGAAGAGAGAGGAGCGATGGGACCAAGCTGGACCCAGCTGGACCGGAGGTGA 420
Qy 421 AAGAGAAAGAGACTGGAGACAAACAAAGAGAAAGATTGGAGCGGACCAAGTCTCAGCAGCC 480

421	Db	 AAGAGAGAAAGACTTGGAGACAAACAAAGAGAAGATTTGGAGCGCAACCAAGTTCATCAGCAGCC	480
481	Qy	ACGGAAAAATAGGCCCGGAAGAGAGAAAGAGAAACAAAGATGGGGAAACACACAGGTAGCCA	540
481	Db	ACGGAAAAATAGGCCCGGAAGAGAGAAAGAGAAACAAAGATGGGGAAACACACAGGTAGCCA	540
541	Qy	TGTGAGGGAAGAAACATCTCCGAAACAAACCTTTCTACTTCCCGTCGAAGCGGTTTAGCAC	600
541	Db	TGTGAGGGAAGAAACATCTCCGAAACAAACCTTTCTACTTCCCGTCGAAGCGGTTTAGCAC	600
601	Qy	CCGCTACGGGAAACAAAAACGGTAGGATCCGGTCTCTCAGAGGTTTGACCAAAGGTCGAAG	660
601	Db	CCGCTACGGGAAACAAAAACGGTAGGATCCGGTCTCTCAGAGGTTTGACCAAAGGTCGAAG	660
661	Qy	GCAGTTTCAGAACTCTCCAGAAATCACCGTATTGTGCAGATCGAGGCCAAACCTTAACACTCT	720
661	Db	GCAGTTTCAGAACTCTCCAGAAATCACCGTATTGTGCAGATCGAGGCCAAACCTTAACACTCT	720
721	Qy	TGTTCTTTCCCAAGCACGCTGATGCTGATAACATCCTTTGTTATCCAGCAAGGGCAAGCCAC	780
721	Db	TGTTCTTTCCCAAGCACGCTGATGCTGATAACATCCTTTGTTATCCAGCAAGGGCAAGCCAC	780
781	Qy	CGTGACCGGTAGCAAAATGGCAATAACAGAAAGAGCTTTTAATCTTTGAACGAGGCCATGCACT	840
781	Db	CGTGACCGGTAGCAAAATGGCAATAACAGAAAGAGCTTTTAATCTTTGAACGAGGCCATGCACT	840
841	Qy	CAGAAATCCCATCCGGTTTCATTTTCTCTACATCTTTGAACCGCCATGACAAACAGAACTCAG	900
841	Db	CAGAAATCCCATCCGGTTTCATTTTCTCTACATCTTTGAACCGCCATGACAAACAGAACTCAG	900
901	Qy	AGTAGCTAAAAATCTCCATGCGCGTTAAACACACCCGGCCAGTTTGAGGATTTCTTCCCGCG	960
901	Db	AGTAGCTAAAAATCTCCATGCGCGTTAAACACACCCGGCCAGTTTGAGGATTTCTTCCCGCG	960
961	Qy	GAGCAGCCGAGACCAATCATCTTACTTTGCAGGGCTTCAGCAGGAATACGTTTGAGAGCCGC	1020
961	Db	GAGCAGCCGAGACCAATCATCTTACTTTGCAGGGCTTCAGCAGGAATACGTTTGAGAGCCGC	1020
1021	Qy	CTTTCAAATCCGGAAATTCATCAGATACCGAGGGTGCTGTTAGAGAGAAATCGAGAGGTGA	1080
1021	Db	CTTTCAAATCCGGAAATTCATCAGATACCGAGGGTGCTGTTAGAGAGAAATCGAGAGGTGA	1080
1081	Qy	GCAAGAGGAGAGGGGCAGAGGCATCGAGTACTCGGAGTAGTGAGAAACAAATCAAGGAGT	1140
1081	Db	GCAAGAGGAGAGGGGCAGAGGCATCGAGTACTCGGAGTAGTGAGAAACAAATCAAGGAGT	1140
1141	Qy	GATAGTCAAAAGTGTCAAAGGAGCAGTTGTAAGAACTTTACTAAGCACGCTAAATCCGFTCT	1200
1141	Db	GATAGTCAAAAGTGTCAAAGGAGCAGTTGTAAGAACTTTACTAAGCACGCTAAATCCGFTCT	1200
1201	Qy	AAAGAAAGGCTCCGAAAGAGAGGAGATATCAACCAACCAATCAACTTGAGAGAAAGCCGA	1260
1201	Db	AAAGAAAGGCTCCGAAAGAGAGGAGATATCAACCAACCAATCAACTTGAGAGAAAGCCGA	1260
1261	Qy	GCCCGATCTTTCTAAACAACTTTGGGAAGTTATTGAGGTGAGCCACACAAGAAAGAACCC	1320
1261	Db	GCCCGATCTTTCTAAACAACTTTGGGAAGTTATTGAGGTGAGCCACACAAGAAAGAACCC	1320
1321	Qy	CCAGCTTCAGGACCTGGACATGATGCTCACTGTTGTAGAGATCAAGAAAGGAGCTTTGAT	1380
1321	Db	CCAGCTTCAGGACCTGGACATGATGCTCACTGTTGTAGAGATCAAGAAAGGAGCTTTGAT	1380
1381	Qy	GCTCCCACTTTCAACTCAAAGGCCATGGTTATCGTCGTCTGTCNAACAAAGAACTGGAAA	1440
1381	Db	GCTCCCACTTTCAACTCAAAGGCCATGGTTATCGTCGTCTGTCNAACAAAGAACTGGAAA	1440
1441	Qy	CTTTGAATCTCGTGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGAAGAGAGGA	1500
1441	Db	CTTTGAATCTCGTGCTGTAAAGAAAGAGCAACACAGAGGGGACGGCGGAAGAGAGGA	1500
1501	Qy	GGACGAAGACGAAGAGAGGGAAGTAAACAGAGAGTTCGTAGGTATACACGCGAGTTT	1560

1501	DB	GGACGAAGCGAAGAGAGGAGGGAAGTAACACAGAGGTGCGTAGGTACACACCGAGGTT	1560
1561	QY	GAAGGAAGCGATGTGTTTCATCATGCGCAGAGCTCATCCAGTAGCCATCAAGCGTTTCCTC	1620
1561	DB	GAAGGAAGCGATGTGTTTCATCATGCGCAGAGCTCATCCAGTAGCCATCAAGCGTTTCCTC	1620
1621	QY	CGAACTCCATCTCGTTGGCTTCGGTATCAACGCTGAAACACACACAGAACTCTTCCTTGC	1680
1621	DB	CGAACTCCATCTCGTTGGCTTCGGTATCAACGCTGAAACACACAGAACTCTTCCTTGC	1680
1681	QY	AGGTGATAAGGACAAATGCTGATAGACACAGATAGAGAAGCAAGCGAAGGATTTAGCATTCCTC	1740
1681	DB	AGGTGATAAGGACAAATGCTGATAGACACAGATAGAGAAGCAAGCGAAGGATTTAGCATTCCTC	1740
1741	QY	TGGGTGGGTGAACAAAGTTTGAGAAAGCTCATCAAAAAACAGAGGAATCTCATTGTGTAG	1800
1741	DB	TGGGTGGGTGAACAAAGTTTGAGAAAGCTCATCAAAAAACAGAGGAATCTCATTGTGTAG	1800
1801	QY	TGCTCGTCCTCAATCTCAATCTCCGTCGTCCTGAGAAAGAGTCTCCTCAGAGAA	1860
1801	DB	TGCTCGTCCTCAATCTCAATCTCCGTCGTCCTGAGAAAGAGTCTCCTCAGAGAA	1860
1861	QY	AGAGGATCAAGAGGAGGAGAAAAACCAAGAGGGAAGGTCCTCCTTTTGAAGGC	1920
1861	DB	AGAGGATCAAGAGGAGGAGAAAAACCAAGAGGGAAGGTCCTCCTTTTGAAGGC	1920
1921	QY	TTTTTAAGTGAAGTGGAGGCAACTGCTGTATGATATCGATATATAGATACAGCTTTTGTACT	1980
1921	DB	TTTTTAAGTGAAGTGGAGGCAACTGCTGTATGATATCGATATATAGATACAGCTTTTGTACT	1980
1981	QY	CTACTATCCAAAAACTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC	2032
1981	DB	CTACTATCCAAAAACTTATCAATAAATAAAAAAGTTTGTGCGTTGTTTCTCC	2032

RESULT 5

US-09-106-872A-3

; Sequence 3, Application US/09106872A

; Patent No. 6486311

GENERAL INFORMATION:

; APPLICANT: Burks Jr., A. Wesley

APPLICANT: Stanley, J. Steven

; APPLICANT: Cockrell, Gael

APPLICANT: King, Nina E.

APPLICANT: Sampson, Hugh A.

APPLICANT: Helm, Ricki M.

APPLICANT: Bannion, Gary A.

; TITLE OF INVENTION: peanut Allergens and Methods

FILE REFERENCE: HS 103 CIP
CURRENT ADDICTION NUMBER:

; CURRENT APPLICATION NUMBER: US/09/106,874A
 : CURRENT FILING DATE: 1999-06-29

; CURRENT FILING DATE: 1993-06-23
 ; PRIOR APPLICATION NUMBER: PCT/US

; PRIOR APPLICATION NUMBER: FCI/0390/15222
; PRIOR FILING DATE: 1996-09-23

; PRIOR FILING DATE: 1998-03-23
 : NUMBER OF SEQ ID NOS: 23

: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Patent In Ver.

: SEO ID NO 3

: LENGTH: 1930

TYPE: DNA

ORGANISM: *Arachis hypogaea*

US-09-106-872A-3

Query Match 95.0%; Score 1930; DB 3; Length 1930;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1930;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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121 TGCCAGTCAATCACTTTACAGAGAAAGAAACAGAGAAACCCCTCGGCCCCAGAGGTGCCTCCA 180
181 GAGTTGTCAACAGAAACCGGATGACTTTGAAGCAAAAGGCATCGAGTCTCGCTGCACCAA 240
181 GAGTTGTCAACAGAAACCGGATGACTTTGAAGCAAAAGGCATCGAGTCTCGCTGCACCAA 240
241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCTCTCGAGGACACACTGGCACCAACCAACCA 300
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301 ACCTTCCCTCCAGGGAGCGGACACCTGGCCGCAACCCGAGACTACGATGATGACCG 360
361 CCCTCAACCCCGAGAGAGAGAGAGCCGATGGGACACAGCTGGACCCGAGGGAGCGTGA 420
361 CCCTCAACCCCGAGAGAGAGAGAGCCGATGGGACACAGCTGGACCCGAGGGAGCGTGA 420
421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGGCGACCAAGTCACTCAGCAGCC 480
421 AAGAGAAAGAGACTGGAGACAAACAGAGAAAGATTGGAGGCGACCAAGTCACTCAGCAGCC 480
481 ACAGAAATTAAGCCCGAGAGAGAGAGAGAGAAACAGAGTGGGGAAACACAGGTAGCCA 540
481 ACAGAAATTAAGCCCGAGAGAGAGAGAGAGAAACAGAGTGGGGAAACACAGGTAGCCA 540
541 TGTGAGGAGAAACATCTCGGAACACCCCTTTCTACTTCCCTCAAGGCGGTTTAGCAC 600
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601 CCCTACCGGAAACAAAACCGTAGGATCCGGGCTCTGCAGAGGTTTGACCAAAAGGTCAAG 660
601 CCCTACCGGAAACAAAACCGTAGGATCCGGGCTCTGCAGAGGTTTGACCAAAAGGTCAAG 660
661 GCAGTTTCAGAAATTCAGAAATCAACAGAAAGAGCTTTAATCTTTGACAGAGGCGCAACTCT 720
661 GCAGTTTCAGAAATTCAGAAATCAACAGAAAGAGCTTTAATCTTTGACAGAGGCGCAACTCT 720
721 TGTTCTTCCCAAGCAGCTGATGCTGATACATCTCTGTTATCCAGCAAGGCGCAAGCCAC 780
721 TGTTCTTCCCAAGCAGCTGATGCTGATACATCTCTGTTATCCAGCAAGGCGCAAGCCAC 780
781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTGACAGAGGCGCAACT 840
781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTGACAGAGGCGCAACT 840
841 CAGAAATCCCATCCGGTTTCATTTCTACATCTTTGAAACCGCCATGACAAACAGAAACCTCAG 900
841 CAGAAATCCCATCCGGTTTCATTTCTACATCTTTGAAACCGCCATGACAAACAGAAACCTCAG 900
901 AGTAGCTAAATCTCCATGCCGTTTAAACACACCGGCCAGTTTGAGGATTTCTTCCCGGC 960
901 AGTAGCTAAATCTCCATGCCGTTTAAACACACCGGCCAGTTTGAGGATTTCTTCCCGGC 960
961 GAGCAGCCGAGACCAATCACTCTTCTGAGGCTTTCAGCAGGAATACGTTGGAGGCGGC 1020
961 GAGCAGCCGAGACCAATCACTCTTCTGAGGCTTTCAGCAGGAATACGTTGGAGGCGGC 1020
1021 CTTCAATCGGAAATCAATGAGATA CGGAGGGTCTGTTAGAGAGAAATGCGAGGAGTGA 1080
1021 CTTCAATCGGAAATCAATGAGATA CGGAGGGTCTGTTAGAGAGAAATGCGAGGAGTGA 1080
1081 GCAAGAGGAGAGGCGCAGGCGATGAGTACTCGAGTCTGAGCAACAAAGAGT 1140
1081 GCAAGAGGAGAGGCGCAGGCGATGAGTACTCGAGTCTGAGCAACAAAGAGT 1140
1141 GATAGTCAAAAGTCAAAAGAGCAGCTTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTC 1200
1141 GATAGTCAAAAGTCAAAAGAGCAGCTTTGAAGAACTTACTTAAGCAGCGCTAAATCCGCTC 1200
1201 AAAGAAAGGCTCCGAAAGAGAGGGAGATATACCAACCCCAATCAACTTGAGAGAGGCGA 1260

1201 AAAGAAAGGCTCCGAAAGAGAGGAGATATCA CCAACCCCAATCAACTTGAGAGAGGCGA 1260
1261 GCCCGATCTTTCTAA CAACTTTGGGAGTTATTGGAGTGAAGCCAGACAGAGAACCC 1320
1261 GCCCGATCTTTCTAA CAACTTTGGGAGTTATTGGAGTGAAGCCAGACAGAGAACCC 1320
1321 CCAGCTTCAGGACCTGACATGATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
1321 CCAGCTTCAGGACCTGACATGATGCTCACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
1381 GCTCCACACTTCAACTCAAAAGGCCATGTTATCGTCTGTCTCAACAAAGAGAACTGAAA 1440
1381 GCTCCACACTTCAACTCAAAAGGCCATGTTATCGTCTGTCTCAACAAAGAGAACTGAAA 1440
1441 CTTTGAACCTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAGGGA 1500
1441 CTTTGAACCTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAGGGA 1500
1501 GGACGAAGACGAAAGAGAGAGGAAAGTAAACAGAGAGGTCGCTAGGTACACAGCGAGGTT 1560
1501 GGACGAAGACGAAAGAGAGAGGAAAGTAAACAGAGAGGTCGCTAGGTACACAGCGAGGTT 1560
1561 GAAGGAAGGCGATGTTTCATCATGTCAGCAGCTCATCTCCAGTACGAGTCAACCGCTTCTC 1620
1561 GAAGGAAGGCGATGTTTCATCATGTCAGCAGCTCATCTCCAGTACGAGTCAACCGCTTCTC 1620
1621 CGAACTCCCATCTCGTTGGCTTCCGTTATCAACGCTGAAACAAACACAGAAATCTTCTTGC 1680
1621 CGAACTCCCATCTCGTTGGCTTCCGTTATCAACGCTGAAACAAACACAGAAATCTTCTTGC 1680
1681 AGTGATAAGGCAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTTAGCATTTCCC 1740
1681 AGTGATAAGGCAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTTAGCATTTCCC 1740
1741 TGGGTCGGGTGAACAAAGTTGAGAGGCTCATCAAAAAACAGAGGAATCTCACTTTGTGAG 1800
1741 TGGGTCGGGTGAACAAAGTTGAGAGGCTCATCAAAAAACAGAGGAATCTCACTTTGTGAG 1800
1801 TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 1860
1801 TGCTCGTCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCTCAATCT 1860
1861 AGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
1861 AGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
1921 TTTTAACTGA 1930
1921 TTTTAACTGA 1930

RESULT 6

US-09-106-872A-19

; Sequence 19, Application US/09106872A

; Patent No. 6486311

; GENERAL INFORMATION:

; APPLICANT: Burks Jr., A. Wesley

; APPLICANT: Stanley, J. Steven

; APPLICANT: Cockrell, J. Gael

; APPLICANT: King, Nina E.

; APPLICANT: Sampson, Hugh A.

; APPLICANT: Helm, Ricki M.

; APPLICANT: Bannon, Gary A.

; TITLE OF INVENTION: Peanut Allergens and Methods

; FILE REFERENCE: HS 103 CIP

; CURRENT APPLICATION NUMBER: US/09/106,872A

; CURRENT FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: PCT/US96/15222

; PRIOR FILING DATE: 1996-09-23

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO 19


```
RESULT 7
US-09-191-593-4
; Sequence 4, Application US/09191593
; Patent No. 6835824
; GENERAL INFORMATION:
; APPLICANT: BURKS, A Wesley, HELM, Ricki M,
; APPLICANT: COCKRELL, Gael, STANLEY, J Steven,
; APPLICANT: BANNON, Gary A
; TITLE OF INVENTION: PEANUT ALLERGENS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Head, Johnson & Kachigian
; STREET: 112 W. Center St., Suite 230
; CITY: Fayetteville
; STATE: Arkansas AR
; COUNTRY: United States of America
; ZIP: 72701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Wordperfect 6.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,593
; FILING DATE: 13 NOVEMBER 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/717,933
; FILING DATE: 23 SEPTEMBER 1996
; APPLICATION NUMBER: US 07/998,377
; FILING DATE: 30 DECEMBER 1992
; APPLICATION NUMBER: US 08/158,704
; FILING DATE: 29 NOVEMBER 1993
; APPLICATION NUMBER: US 60/009,455
; FILING DATE: 29 DECEMBER 1995
; APPLICATION NUMBER: US 08/610,424
; FILING DATE: 04 MARCH 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ALEXANDER, DANIEL R
; REGISTRATION NUMBER: 32,604
; REFERENCE/DOCKET NUMBER: ARK00895601B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (501) 582-9111
; TELEFAX: (501) 521-4931
; TELEX: No. 6835824 applicable
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1949 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; DESCRIPTION: identified as Ara h I Alpha P17
; HYPOTHEetical: No
; ANTI-SENSE: No
; FRAGMENT TYPE: No. 6835824 applicable
; ORIGINAL SOURCE:
; ORGANISM: Arachis hypogaea
; STRAIN: Florunner
; INDIVIDUAL ISOLATE: Clone P17
; DEVELOPMENTAL STAGE: Seed
; HAPLOTYPE: No. 6835824 applicable
; TISSUE TYPE: Seed mRNA, cDNA library
; CELL TYPE: No. 6835824 applicable
; CELL LINE: No. 6835824 applicable
; ORGANELLE: No. 6835824 applicable
; IMMEDIATE SOURCE:
; LIBRARY: Florunner seed cDNA expression
; LIBRARY: library in Uni-ZAP XR vector
; CLONE: P17
; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: No. 6835824 applicable
; MAP POSITION: No. 6835824 applicable
; UNITS: No. 6835824 applicable
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1847
; IDENTIFICATION METHOD: By agreement with
; IDENTIFICATION METHOD: protein information and established
; IDENTIFICATION METHOD: consensus sequence
; OTHER INFORMATION: Seed storage protein and
; OTHER INFORMATION: allergen
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-09-191-593-4

Query Match 86.2%; Score 1752.4; DB 3; Length 1949;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches 46; Indels 54; Gaps 6;

Qy 48 CAATGAGAGGGGGTTTCTCCACTGATGCTGTGTAGGGATCTTGTCTCGCTTCAG 107
Db 1 CAATGAGAGGGGGTTTCTCCACTGATGCTGTGTAGGGATCTTGTCTCGCTTCAG 60
Qy 108 TTCTCGCAACGCGATGCCAAGTCACTTACCAGAAAGAAAACAGAGAACCCCTGCCGCC 167
Db 61 TTCTCGCAACGCGAGGCCAAGTCACTTACCAGAAAGAAAACAGAGAACCCCTGCCGCC 114
Qy 168 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCCGATGACTTTGAAGCAAAAGCGATGCGAGT 227
Db 115 AGAGGTGCTCTCCAGAGTTGTCAACAGGAACCCGATGACTTTGAAGCAAAAGCGATGCGAGT 174
Qy 228 CTCGCTGCACCAAGCTCGAGTATGATCTCGTTGTGTCTATGATCTCTCGAGGACACACTG 287
Db 175 CTCGCTGCACCAAGCTCGAGTATGATCTCGTTGTGTCTATG-----ACACTG 222
Qy 288 GCACCAACCAACCAACGTTCCCTCCAGGGAGCGGACACGTCGCCGCCAACCCGGAGACT 347
Db 223 GCGCCACCAACCAACGTTCCCTCCAGGGAGCGGACACGTCGCCGCCAACCCGGAGACT 282
Qy 348 ACATGATGACCGCGCTCAACCCCGAAGAGAGGAAGCGCCGATGGGACCGAGCTGGAC 407
Db 283 ACATGATGACCGCGCTCAACCCCGAAGAGAGGAAGCGCCGATGGGACCGAGCTGAAC 342
Qy 408 CGAGGAGCGTGAAGAGAGAAAGACTGGAGACAACCAAGAGAGATTTGAGGCGGACCAA 467
Db 343 CGAGGAGCGTGAAGAGAGAAAGACTGGAGACAACCAAGAGAGATTTGAGGCGGACCAA 402
Qy 468 GTCATCAGCAGCCACCGAAAATAAGCCCGAAGAGAGAGAGAAAGAGAGTGGGGAA 527
Db 403 GTCATCAGCAGCCACCGAAAATAAGCCCGAAGAGAGAGAGAGAGAGTGGGGAA 462
Qy 528 CACCAAGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAA 587
Db 463 CACCAAGTAGCCATGTGAGGGAAGAAACATCTCGGAACAAACCCCTTCTACTTCCCGTCAA 522
Qy 588 GCGGTTTACACCCCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGCAGAGTTTG 647
Db 523 GCGGTTTACACCCCTACGGGAACCAAAACGGTAGGATCCGGGTCTCTGCAGAGTTTG 582
Qy 648 ACCAAAGGTCAAGGCGATTTTCAAGATCTCCAGAAATCACCGTATTTGTCAGATCGAGCCA 707
Db 583 ACCAAAGGTCAAGGCGATTTTCAAGATCTCCAGAAATCACCGTATTTGTCAGATCGAGCCA 642
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QY 708 AACCTAACACTCTTGTCTTCCCAAGCAGCGTGTATGATCAATCCTTGTATCCAGC 767
DB 643 GACCTTAACACTCTTGTCTTCCCAAGCAGCGTGTATGATCAATCCTTGTATCCAGC 702
QY 768 AAGGCGAAGCAGCGTGTATGATCAATGCGCAATTAACGAAAGAGAGCTTTAATCTTGTAGC 827
DB 703 AAGGCAAGCAGCGTGTATGATCAATGCGCAATTAACGAAAGAGAGCTTTAATCTTGTAGC 762
QY 828 AGGCGCATGCACTCAGAAATCCCATCCGTTTCAATCTTCTACATCTTTGAACCGCCATGACA 887
DB 763 AGGCGCATGCACTCAGAAATCCCATCCGTTTCAATCTTCTACATCTTTGAATCGACATGACA 822
QY 888 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCGGTTAAACACACCGCGCAGTTTGAGG 947
DB 823 ACCAGAACCTCAGAGTAGCTAAATCTCCATGCGGTTAAACACCGCGCGCAGTTTGAGG 882
QY 948 ATTCTCTCCGCGGAGCAGCGGAGACCAATCATCTTCTTGTGAGGCTTCAGCAGGAATA 1007
DB 883 ATTCTCTCCGCGGAGCAGCGGAGACCAATCATCTTCTTGTGAGGATTCAGCAGGAATA 942
QY 1008 CGTTGAGGCGCGCTTCAATGCGGAATTCATGAGATACGAGGGTGTCTTTAAGAGAGA 1067
DB 943 CTTTGGAGGCGCGCTTCAATGCGGAATTCATGAGATACGAGGGTGTCTTTAAGAGAGA 1002
QY 1068 ATGCAAGGTTGACGAGAGGAGAGGCGGAGGCGATGGAGTACTCGGAGTAGTGAGA 1127
DB 1003 ATGCAAGGAGAGAGGAGAGGAGGCGGAGGCGAGGAGTACTCGGAGTAGTG--- 1059
QY 1128 ACAATGAAGGAGTAGTAGTCAAAAGTGTCAAAGGAGCACGTTGAAGAACTTACTAAGCACG 1187
DB 1060 ATAATGAAGGAGTAGTAGTCAAAAGTGTCAAAGGAGCACGTTCAAGAACTTACTAAGCACG 1119
QY 1188 CTAATCTCCGTCTCAAGAAAGGCTCCGAGAGAGGAGATATCAACCAACCCCAATCAACT 1247
DB 1120 CTAATCTCCGTCTCAAGAAAGGCTCC---GAAGAGGAAGATATCAACCAACCCCAATCAACT 1176
QY 1248 TGAGAGAGGCGAGCGGATCTTCTTCAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1307
DB 1177 TGAGAGATGCGGAGCGGATCTTCTTCAACAACTTTGGGAAGTTATTTGAGGTGAAGCCAG 1236
QY 1308 ACAAGAGAAACCCCAAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAAAG 1367
DB 1237 ACAAGAGAAACCCCAAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAG 1296
QY 1368 AAGGAGCTTTGATGCTCCACACTTCAAAAGGCGCATGGTTATCGTGTGCTCAACA 1427
DB 1297 AAGGAGCTTTGATGCTCCACACTTCAAAAGGCGCATGGTTCATCGTGTGCTCAACA 1356
QY 1428 AAGGAACTGGAAACCTTGAACTCGTGTGTAAGAAAGAGCAACACAGAGGGGACGGC 1487
DB 1357 AAGGAACTGGAAACCTTGAACTCGTGTGTAAGAAAGAGCAACACAGAGGGGACGGC 1416
QY 1488 GGGAA-----GAAGAGGAGGACGAAGCAAGAGAGGAGGAAAGTAACAGAGAGG 1538
DB 1417 GGGAAAGAGTGGGAAGAGAGAGGAGAGATGAAGAGAGGAGGAGTAACAGAGAGG 1476
QY 1539 TCGGTAGGTACACAGCGAGTTGAAGAGGCGATGTGTTCATGTATGCGCAGAGCTCATC 1598
DB 1477 TCGGTAGGTACACAGCGAGTTGAAGAGGCGATGTGTTCATGTATGCGCAGAGCTCATC 1536
QY 1599 CAGTAGCCATCAAGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAAGCTGAAA 1658
DB 1537 CAGTAGCCATCAAGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAAGCTGAAA 1596
QY 1659 ACAACACAGAACTTCTTCTTGCAGGTGATAAGGACAAATGTATGATAGACCAGATAGAGAAGC 1718
DB 1597 ACAACACAGAACTTCTTCTTGCAGGTGATAAGGACAAATGTATGATAGACCAGATAGAGAAGC 1656
QY 1719 AAGCGAAGATTTAGCATTCCTTGGGTGCGGTGAAACAAAGTTGAGAGCTCATCAAAAACC 1778
DB 1657 AAGCGAAGATTTAGCATTCCTTGGGTGCGGTGAAACAAAGTTGAGAGCTCATCAAAAACC 1716
QY 1779 AGAAGGAATCTCACTTTGTGAGTGCTCGTCTCTCAATCTCAATCTCTCCGTCGCTC 1838

DB 1717 AGAGGAGAGTCTCACCTTTGTGAGTGTCTCGCTCAATCTCAATCTCGTCTC----- 1765
QY 1839 CTGAGAAAAGAGTCTCTCTGAGAAAAGAGATCAAGAGAGGAGAAAACCAAGAGGAGGAGGTC 1898
DB 1766 -----GTCTCTCTGAAAAGAGGATCAAGAGGAGGAAAACCAAGAGGAGGAGGTC 1815
QY 1899 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTGTATGTATCGAT 1958
DB 1816 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCGAT 1875
QY 1959 AATAAGATCACGCTTTTGTACTCTACTATCCAAAACCTTATCAATAAATAAATAACCGTTTG 2018
DB 1876 AATAAGATCACGCTTTTGTAACTACTATCCAAAACCTTATCAATAAATAAATAACCGTTTG 1935
QY 2019 TCGTGTGTCTTCTCC 2032
DB 1936 TCGTGTGTCTTCTCC 1949

RESULT 8
US-09-106-872A-18
; Sequence 18, Application US/09106872A
; Patent No. 6496311
; GENERAL INFORMATION:
; APPLICANT: Burks Jr., A. Wesley
; APPLICANT: Stanley, J. Steven
; APPLICANT: Cockrell, Gael
; APPLICANT: King, Nina E.
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Helm, Ricki M.
; APPLICANT: Bannion, Gary A.
; TITLE OF INVENTION: Peanut Allergens and Methods
; FILE REFERENCE: HS 103 CIP
; CURRENT APPLICATION NUMBER: US/09/106,872A
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: PCT/US96/15222
; PRIOR FILING DATE: 1996-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-09-106-872A-18

Query Match 36.9%; Score 750; DB 3; Length 750;
Best Local Similarity 100.0%; Pred. No. 2.3e-217;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 687 GTATTGTGCAGATCGAGGCCAAACCTTAACACTCTTGTCTTCCCAAGCAGCGTGTGCTG 746
DB 1 GTATTGTGCAGATCGAGGCCAAACCTTAACACTCTTGTCTTCCCAAGCAGCGTGTGCTG 60
QY 747 ATAACATCCTTGTATCTCAGCAAGGCAAGCCAGCGTAGCAAAATGGCAATAACA 806
DB 61 ATAACATCCTTGTATCTCAGCAAGGCAAGCCAGCGTAGCAAAATGGCAATAACA 120
QY 807 GAAAGAGCTTTAATCTTGTGAGGGCCATGCAATCTCAGAAATCCCGTTCATTTCTCT 866
DB 121 GAAAGAGCTTTAATCTTGTGAGGGCCATGCAATCTCAGAAATCCCGTTCATTTCTCT 180
QY 867 ACATCTTGAACCGCCATGACACCAAGACTCAGAGTAGCTAAAATCTCATGCCCCGTTA 926
DB 181 ACATCTTGAACCGCCATGACACCAAGACTCAGAGTAGCTAAAATCTCATGCCCCGTTA 240
QY 927 ACACACCCCGCCAGTTTGTAGGATTTCTTCCCGCGAGCAGCGAGACCAATCATCTCTACT 986
DB 241 ACACACCCCGCCAGTTTGTAGGATTTCTTCCCGCGAGCAGCGAGACCAATCATCTCTACT 300
QY 987 TCGAGGGCTTCAGCAGGAATACTGTGGAGGCGCGCTTCAATGCGGAATTCATGAGATAC 1046
DB 301 TCGAGGGCTTCAGCAGGAATACTGTGGAGGCGCGCTTCAATGCGGAATTCATGAGATAC 360

QY 1047 GGAGGGTCTGTTTAAAGAGAAATCGAGGAGGTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAT 1106
DB 361 GGAGGGTCTGTTTAAAGAGAAATCGAGGAGGTGAGCAAGAGGAGGAGGAGGAGGAGGAT 420
QY 1107 GGAGTACTCGAGTAGTGAGAACAAATGAAGAGGTAGTAGTCAAAAGTGTCAAAAGAGCAAG 1166
DB 421 GGAGTACTCGAGTAGTGAGAACAAATGAAGAGGTAGTAGTCAAAAGTGTCAAAAGAGCAAG 480
QY 1167 TTGAAGAACTTACTTAAGCAGCTAAATCCGCTCTCAAAAGAAAGGCTCCGAAAGAGAGGAG 1226
DB 481 TTGAAGAACTTACTTAAGCAGCTAAATCCGCTCTCAAAAGAAAGGCTCCGAAAGAGAGGAG 540
QY 1227 ATATCAACAAACCCCAATCAACTTTGAGAAAGCGAGCCGATCTTTCTTAAACAACTTTGGGA 1286
DB 541 ATATCAACAAACCCCAATCAACTTTGAGAAAGCGAGCCGATCTTTCTTAAACAACTTTGGGA 600
QY 1287 AGTTATTTGAGGTGAAGCCAGACAAAGAAAGAACCCCAAGCTTTCAGGACCTGGACATGATGC 1346
DB 601 AGTTATTTGAGGTGAAGCCAGACAAAGAAAGAACCCCAAGCTTTCAGGACCTGGACATGATGC 660
QY 1347 TCACCTGTGTAGATCAAGAGAGGAGCTTTGATGCTCCACACTTCAACTCAAGAGGCA 1406
DB 661 TCACCTGTGTAGATCAAGAGAGGAGCTTTGATGCTCCACACTTCAACTCAAGAGGCA 720
QY 1407 TGGTTATCGTCTGCTCAACAAAGGAACTG 1436
DB 721 TGGTTATCGTCTGCTCAACAAAGGAACTG 750

RESULT 9

US-10-245-227D-84
; Sequence 84, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadig, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245, 227D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 84
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Glycine max
US-10-245-227D-84

Query Match 20.1%; Score 408.4; DB 3; Length 1350;
Best Local Similarity 62.2%; Pred. No. 3e-113;
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAACCTTCTACTT---CCCGTCAAGCGGTTTAGACCCGCTACGGGACCAAAA 618
DB 120 GAATAACCTTCTACTTTAGAGAGCTTAAACGCTTCCAAACTCTCTTTGAGAAACAAA 179
QY 619 CGGTAGGATCCGGGTCTCTGAGAGGTTTGAACCAAGGTCAAGGCAGTTTCAGAACTCTCCA 678
DB 180 CGGTGCGATTCTGCTCATTACAGAGATTCAACAAACGCTCCCAACACTTGAGAACCTTCG 239
QY 679 GAATACCGTATTGTGAGATCGAGGCCAAACCTTAACACTCTTTGTTCTTCCCAAGCAGCG 738
DB 240 AGACTACCGATTGTCTCAGTTTCAGTCAAAACCAACACAAATCATTTCTCCCCCAACATGC 299
QY 739 TGATGCTGATAACATCTCTGTTATCCAGCAAGGCGACCCAGCTGACCGTAGCAATGG 798
DB 300 TGACGCGGATTTCATTATTATTATTTCTTAGCGGAGAGCCATACTTACCTTTGTGAACAA 359
QY 799 CAATAACAGAAAGAGCTTTTAACTTTCAGGAGGCGCATGCACTCAGAAATCCCATCCCGTTT 858

DB 360 CGACGACAGAGACTCTCTACAACATTTCCACCTGGCGATGCCAGAGAAATCCACAGCTGGAAC 419
QY 859 CATTTCTTACATCTTGAACCGCCATGACAACACAGAACTCAGAGTAGCTAAATCTCCAT 918
DB 420 CACTTACTATATTATTAAACCTTCAACGACCAAGAAATCTCAAAATAATCAAAATTTGCCAT 479
QY 919 GCCCGTTTAAACACACCCCGGCGAGTTTGAAGATTCTTCCCGCGAGCAGCAGAGCAATC 978
DB 480 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 539
QY 979 ATCTTACTTCCAGGGCTTTCAGCAGGAATACGTTGGAGCGCCCTTCAATCGGAATTTCAA 1038
DB 540 GTCTTACTTCAAGGGCTTTCAGCCATAATATTCTAGAGACCTCTCTTCCATAGCGAAATTCGA 599
QY 1039 TGAGATACGAGGGTGTCTGTAGNAGAGATGCAAGAGGTGACCAAGAGCAGAGAGGCA 1098
DB 600 GGAGATAAACAGGGTTTGTGGAGAGGAAGAGGAGCAGAGGCGCAAGAG----- 651
QY 1099 GAGGCGATGAGTACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAAAGTGTCAAA 1158
DB 652 -----GGAGTGTCTGGAATCTCTCAAA 674
QY 1159 GGAGCAGCTTTGAAGAACTTACTAAGCAGCTAAATCCGTCTCAAAAGAAAGCTCCGAAGA 1218
DB 675 GGAACAAATTCGGCAACTGAGCAGCGTGCATAATCTAGTTCAAGGAAACCACTTCTCCTC 734
QY 1219 AGAGGAGATATCACCAACCAATCACTTGAAGAGGCGAGCCCGATCTTTCTTAACAA 1278
DB 735 CGAAGATG-----AACCTTCAACTTGAAGCGCGCAACCCCATCTATTTCACAA 785
QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCAGACAAAGAAACCCCGAGCTTCAGGACCTGGA 1338
DB 786 CTTTGGAAAGTTCTTTGAGATCACCCTG---AGAAAAACCCACAGCTTCGGNCTTGGGA 842
QY 1339 CATGATGCTCACTGTGTAGAGATCAAAAGAGGCTTTGATGCTCCCACTTTCAACTC 1398
DB 843 TATCTTCTCAGTTCTGTGGATATCAACGAAGGAGCTCTTCTTCTACCACTTCAATTC 902
QY 1399 AAAGGCGATGTTATCGTCTGCTCAACAAAGAACTGGNAACTTTGAACCTCGGCTGT 1458
DB 903 AAAGGCGATGATGATAGTACTAGTGATTAATGAAGAGAGATGCAAAACATTGAACTTGTGGCAT 962
QY 1459 AAGAAAAGAGCAACACAGAGGCGCGCGGGAAGAGAGGAGGAGCAACGACGAAGAAGA 1518
DB 963 TAAAGAACACACACAGAGCAAGAAACAGGAGAGGAACTTTG----- 1005
QY 1519 GGAGGAAAGTAAACAGAGAGGTGCTAGGTACACAGCAGAGGTTGAAGGAAGCGGATGTGT 1578
DB 1006 -----GAAGTGCAAAAGGTACAGAGCTGAATTTGCTCAAGACCATGTATT 1049
QY 1579 CATCATGCCAGAGCTCATCCAGTACCATCAACGCTTCTCCGAACCTCATCTGCTTG 1638
DB 1050 TGTAATTCAGCAGAGCTTATCCATTTTGTGCTCAACGCTACCTCAAACTCAATTTCTTGC 1109
QY 1639 CTTTCGGTATCAACGCTGAAAAACCAACACAGAAATCTTCTTCTGAGGTGATGAAGCAATGT 1698
DB 1110 TTTTGGTATCAATGCTTGAGAACCAACAGAGAACTTCTTCTGAGGCGAGAAAGCAATGT 1169
QY 1699 GATAGACAGATAGAGAAGCAAGCGAAGGATTTAGCATTCCTTGGGTGCGGTGAACAAGT 1758
DB 1170 GGTAAAGCGAGATAGAAAGCAAGTGCAGGAGCTTGGTTTCCCTGGGTCTGCAAGATGT 1229
QY 1759 TGAGAGCTCATCAAAACACAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812
DB 1230 TGAGAGGCTATTAAAGAGCAGAGGGAATCTCACTTTGTGATGTCTCAGCTCA 1283

RESULT 10

US-10-245-227D-88
; Sequence 88, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:

; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadi, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245,227D
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 3808
; TYPE: DNA
; ORGANISM: Glycine max
US-10-245-227D-88

Query Match 20.1%; Score 408.4; DB 3; Length 3808;
Best Local Similarity 62.2%; Pred. No. 6e-113;
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAAACCCCTTCTACTTT---CCCGTCAAGCGGTTTAGCACCCGCTACGGGAACCAAAA 618
DB 1293 GAATAACCCCTTCTACTTGAAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAAACCAAAA 1352

QY 619 CGGTAGATCCGGGCTCTGAGAGGTTTGACCAAGGTCNAGGCGATTTTCAGATCTCCA 678
DB 1353 CGGTGCGATTCGCTCTCTCCAGAGATTCAACAAACGCTCCCACTTTGAGAAACCTTCG 1412

QY 679 GAATACCCGATTTGTCAGTTTCAGTCAAAACCCCAACATCTTCTCCCCCACCATGC 738
DB 1413 AGACTACCCGATTTGTCAGTTTCAGTCAAAACCCCAACATCTTCTCCCCCACCATGC 1472

QY 739 TGATGCTGATAACATCTTGTGTTATCCAGCAAGGCGAAGCCGTCGACCGTAGCAATGG 798
DB 1473 TGACGCGATTTCTCTCTCTTCTGCTTAGCGGAGAGCCATCTTACCTTTGTTGAACAA 1532

QY 799 CAATAACAGAAAGCTTTTAATCTTGACGAGGCGCATCTCAGATCCCATCCCGTTT 858
DB 1533 CGACGACAGAGACTCTCTACAACTTCCACCTGCGATGCGCCAGAGAACTCCAGCTGAA 1592

QY 859 CATTTCTACATCTTGAACCGCATGACAAACAGAACTCTCAGATAGCTAAATCTCCAT 918
DB 1593 CACTTACTATTGGTTAACTCTCAGACACAGAGATCTCAAAATATCAAACTTGCAT 1652

QY 919 GCCGTTAACACACCCGCGCATTTGAGGATTTCTTCCGCGAGCAGCGCAGACCAATC 978
DB 1653 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 1712

QY 979 ATCTACTTGCAGGCTTTCAGAGGATACGTTGGAGGCGCTTCAATCGGAATTCAA 1038
DB 1713 GTCTACTTGCAGGCTTTCAGGATATATTTCTAGAGACCTCTCTTCCATAGCGAAATCGA 1772

QY 1039 TGAGATACGAGGCTGCTGTTAGAAAGAGAAATGACAGAGGTGAGCAAGAGAGAGAGGCA 1098
DB 1773 GAGATATAACAGGTTTGTGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1824

QY 1099 GAGGCGATGAGTACTCGGAGTATGAGAAATGAGAGGATGATAGTCAAAAGTGTCAA 1158
DB 1825 -----GGAGTATCTGTGAACTCTCAAA 1847

QY 1159 GGAGCAGTTGAAGAACTTACTAAGCAGCTTAATCGTCTCAAGAAAGGCTCCGAAGA 1218
DB 1848 GGAAACAAATTCGCGAACTAGCAGACGTCGCAATCTAGTTCAAGGAAACCAATTCCTC 1907

QY 1219 AGAGGAGATATCAACAAACCAATCAACTTTGAGAGAGGCGAGCCCGATCTTTCTAACAA 1278
DB 1908 CGAAGATG-----AACCAATCACTTTGAGAGCGCAACCCCATCTATTCCAAACAA 1958

QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAGAAACCCCGAGTTTCCAGACCTGGA 1338
DB 1959 CTTTGGGAAGTTCTTTTGAGATCACCCCTG---AGAAAAACCCCAAGCTTCGGGACTTGA 2015

QY 1339 CATGATGCTCACCTGTGTAGAGATCAAGAAAGGAGCTTTTGATGCTCCCACTTCAACTC 1398
DB 2016 TATCTTCTCAGTTCTGTGGATATCAAGAGAGGCTCTTCTTCTACCACTTCAATTC 2075

QY 1399 AAAGGCCATGGTTATCGTCTGCTCAACAAAGGAACTGGAACCTTTGAACTTCGTGGCTGT 1458
DB 2076 AAAGGCCATAGTCATAGTATGATTAAATGAAGGAGATGCAAACTTGAACCTTTGGCAT 2135

QY 1459 AAGAAAGAGCAACACAGAGGCGCGGAGAAAGAGAGGAGGAGCAAGACGAAGA 1518
DB 2136 TAAAGAAACAAACACAGAGAGCAAGAAACAGGAAGAGGAAACCTTTG----- 2178

QY 1519 GGAGGGAAGTAAACAGAGAGTGTGCTAGGTACACAGCGAGGTTGAAAGAAAGCGGATGTT 1578
DB 2179 -----GAAGTCAAGGTTACAGAGCTGAATGTCTGAAAGCAATGATT 2222

QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCAATCTGTTGG 1638
DB 2223 TGTAAATTCAGCAGCTTATCCATTTGCTCAACGCTACCTCAAACTCAATTTCTTCTGC 2282

QY 1639 CTTGCTATCAACGCTGAAACCAACACAGAACTTCTTTCGAGGTGATAAGCAATGT 1698
DB 2283 TTTTGGTATCAATGCTGAGAAACCAACAGAGGAACTTCTTTCGAGGCGAGAAACAATGT 2342

QY 1699 GATAGACCATAGAGAGCAAGCAAGGATTTAGCATTCCTTGGGTCTGGGTCAACAAGT 1758
DB 2343 GGTAAAGCAGATAGAAAGCAAGTGCAGAGCTTGGTTCCTTGGGTCTGCACAAGATGT 2402

QY 1759 TGAGAAAGCTCATCAAAACCAAGAGAAATCTCACTTTGTGAGTGTCTGCTCTCA 1812
DB 2403 TGAGAGGCTATTAAAGAGCAGAGGGAATCTACTTTGTGATGCTCAGCCTCA 2456

RESULT 11
US-10-245-227D-90
; Sequence 90, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadi, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245,227D
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 3808
; TYPE: DNA
; ORGANISM: Glycine max
US-10-245-227D-90

Query Match 20.1%; Score 408.4; DB 3; Length 3808;
Best Local Similarity 62.2%; Pred. No. 6e-113;
Matches 780; Conservative 0; Mismatches 381; Indels 93; Gaps 5;

QY 562 GAACAAACCCCTTCTACTTT---CCCGTCAAGCGGTTTAGCACCCGCTACGGGAACCAAAA 618
DB 1293 GAATAACCCCTTCTACTTGAAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAAACCAAAA 1352

QY 619 CGGTAGATCCGGGCTCTGAGAGGTTTGACCAAGGTCNAGGCGATTTTCAGATCTCCA 678
DB 1353 CGGTGCGATTCGCTCTCTCCAGAGATTCAACAAACGCTCCCACTTTGAGAAACCTTCG 1412

QY 679 GAATACCCGATTTGTCAGATCCAGGCGAAACCTTAACATCTTCTTCTCCCAAGCAGC 738
DB 1413 AGACTACCCGATTTGTCAGTTTCAGTCAAAACCCCAACATCTTCTCCCCCACCATGC 1472

QY 739 TGATGCTGATAACATCTTGTGTTATCCAGCAAGGCGAAGCCGTCGACCGTAGCAATGG 798

Db 1473 TGACGCGGATTTTCATTATTATTATTCTTAGCGGAGAGCCATACTTACCTTTGGTGAACAA 1532
Qy 799 CAATAACAGAAAGAGCTTTTAACTTTGACAGGGCCATGCACTCAGATCCCATCCGGTTT 858
Db 1533 CGACGACAGAGACTCTTACAACTTCCCTGGCGATGCCAGAGAATCCAGTGGAA 1592
Qy 859 CATTTCTACATCTTGAAACCGCCATGACAAACAGAACTTCAGAGTAGCTAAAATCTCCAT 918
Db 1593 CACTTACTATATTATTAACCTCAGCACCAGAACTCTCAAAATATCAAAATTTGCCAT 1652
Qy 919 GCCGGTTAAACACACCGCCGAGTTTGGAGATTTCTTCCCGGAGAGCCGAGACCAATC 978
Db 1653 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 1712
Qy 979 ATCTCTCTCAGGGCTTTACAGAGAAATACGTTGGAGCGCCCTTCAATCGGAATTCAA 1038
Db 1713 GTCTCTCTCAGGGCTTTACAGCAATATTTCTAGAGACCTCTTCCATAGCAATTCGA 1772
Qy 1039 TGAGATACGGAGGTGCTGTTAGAGAGAAATGCAAGGAGGTGAGCAAGAGAGAGAGGCA 1098
Db 1773 GGAGATAAACAGGGTTTGTGGAGAGGAAGAGAGAGAGGAGGAGCAAGAG----- 1824
Qy 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAGTGTCAAA 1158
Db 1825 -----GGAGTGTATCGTGGAACTCTCAAA 1847
Qy 1159 GGAGCAGGTTGAAGAACTTAAAGCAGCGTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 1848 GGAACAAATTCGGCAACTGAGCAGAGCTGCAAAATCTAGTTCAAGGAAACCAATTTCCCTC 1907
Qy 1219 AGAGGGAGATATCACCAACCCAAATCACTTTGAGAGAAAGGGAGCCGATCTTTCTAACAA 1278
Db 1908 CGAAGATG-----AACCAATTCAGTGAAGCGCAACCCCACTTATTTCCAA 1958
Qy 1279 CTTTGGGAAGTATTTAGAGTGAAGCCAGACAGAAAGAAACCCCGAGCTTCAGAGACTGGA 1338
Db 1959 CTTTGGGAAGTCTTTGAGATACCCCTG---AGAAAAACCCACAGCTTCGGGACTTGA 2015
Qy 1339 CATGATGCTCACCTGTGAGATCAAGAAAGAGCTTTGATGCTCCACACTTCAACTC 1398
Db 2016 TATCTTCTCAGTTCTGTGGATATCAAGAAAGAGCTTCTTCTTACCACACTTCAATTC 2075
Qy 1399 AAAGGCCATGTTATCGTCTGCTGCTCAACAAAGAACTTGAACCTTGAACCTCGTGGCTG 1458
Db 2076 AAAGGCCATGATGATAGTATGATTAATGAAGGAGATGCAACATTTGAACCTTGTGGCAT 2135
Qy 1459 AAGAAAGAGCAACACAGAGGGGACGGCGGGAAGAGAGAGGAGGAGCAAGACGAAGA 1518
Db 2136 TAAAGAAACAAACAGAGAGCAAGAAACAGGAAGAGGAACTTTG----- 2178
Qy 1519 GGAGGGAAGTAAACAGAGAGTGCCTAGGTACACAGGAGGTTGAAGGAAGGCGATGTT 1578
Db 2179 -----GAGTGAAGGTAACAGCTGAATTTGTCTGAAGACCATGATTT 2222
Qy 1579 CATCATGCCAGAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGG 1638
Db 2223 TGTAAATTCAGCAGCTTATCCATTTGCTGCTCAACGCTTACCTCAACCTCAATTTCTTGC 2282
Qy 1639 CTTTCGCTATCAACGCTGAAACAAACACAGAACTTCTTCTGAGGTGATGAAGCAATGT 1698
Db 2283 TTTTGGTATCAATGCTGAGAAACACAGAGGAACTTCTTCTGAGGCGAGAAAGCAATGT 2342
Qy 1699 GATAGACCATAGAGAGCAAGCAAGGATTTAGCAATTCCTTGGGTGCGGTGCAACAGT 1758
Db 2343 GGTAAAGCGATAGAAAGACAAGTGCAGGAGCTTTCGTTCCCTGGGTCTGCAACAGATGT 2402
Qy 1759 TGAGAGCTCATCAAAACACAGAGGAATCTCACTTTGTGAGTCTCGTCTCA 1812
Db 2403 TGAGAGCTTAAAGAGCAGAGGGAATCTTACTTTTGTGATGCTCAGCCTCA 2456

RESULT 12

US-10-245-227D-15

; Sequence 15, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadi, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245, 227D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 15
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mature form of beta-conglycinin beta-subunit
US-10-245-227D-15

Query Match 20.0%; Score 406.8; DB 3; Length 1254;
Best Local Similarity 62.1%; Pred. No. 8.9e-113;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;
Qy 562 GAACAACCCCTTTCTACTT---CCGTCAGGGCGTTTAGCACCCGCTACGGGAACCAAAA 618
Db 24 GAATAACCCCTTTCTACTTTGAGAAGCTCTAACACTTCCAAACTCTCTTTGAGAACCAAAA 83
Qy 619 CGGTAGATCCGGGTCTCTCAGAGTTTGACCAAGGTCAAGGAGTTTCAGAAATCTCCA 678
Db 84 CGGTGCATTCGTCTCTCTCAGAGATTCAACAAACGCTCCCAACAACCTTGAGAACCTTCG 143
Qy 679 GAATCACCGTATTTGTCAGATCGAGCCCAACCTTAACACTCTTTGTTCTTCCCAAGCAGC 738
Db 144 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCCCAACAACCTCTTCTCCCAACCATGC 203
Qy 739 TGATGCTGATAACATCTTGTATCCAGCAAGGCAAGCCAGCCGTCAGCCCTAGCAATGG 798
Db 204 TGACGCGATTTCTCTCTCTTTGCTTACGGGAGAGCCATACTTACTTGTGTGAACA 263
Qy 799 CAATAACAGAAAGAGCTTTAATCTTGACAGGCGCATGCACTCAGAACTCCATCCGTTT 858
Db 264 CGACGACAGAGACTCTTCAACCTTCACTCCCTGGCGATGCCAGAGAATCCAGTGGAA 323
Qy 859 CATTTCTACATCTTCAACCGCATCACAAACCAACCTCAGAGTAGCTAAAATCTCCAT 918
Db 324 CACTTACTATTGGTTTAAACCTTCAACCAACCAAGATCTCAAAATATATCAAACTTGCAT 383
Qy 919 GCCGTTAAACACACCCGCGCAGTTTGAGGATTTTCTCCGCGAGAGCCGAGACCAATC 978
Db 384 ACCGTCACAAACCTTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 443
Qy 979 ATCTTACTTTCAGGGCTTTCAGAGGAATAGTTGGAGGCGCTTCAATCGGAATTCAA 1038
Db 444 GTCTTACTTTCAGAGGCTTTCAGCCATATATTTCTAGAGACTCTCTTCCATAGCAATTCGA 503
Qy 1039 TGAGATACGGAGGTCTGTTAGAGAGATTCAGAGGTTGAGCAAGAGAGAGAGAGGCA 1098
Db 504 GGAGATAAACAGGGTTTGTGGGAGGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
Qy 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAGTGTCAAA 1158
Db 556 -----GGAGTGTCTGGAATCTCAAA 578
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCGTAAATCCGTTCTCAAGAAAGGCTCCGAAGA 1218
Db 579 GGAACAAATTCGGCAACTGAGCAGAGCTGCAAAATCTAGTTCAAGAAACCAATTTCCCTC 638
Qy 1219 AGAGGAGATATCACCAACCAATCACTTGAGAGAGGCGAGCCGCTCTTTCTTCAAA 1278
Db 639 CGAAGATG-----AACCAATTCAGTGAAGAGCCGCAACCCCATCTTATTTCCAAACA 689

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QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAAGAACCCCGAGCTTCAGGACCTGGA 1338
Db 690 CTTTGGAAAGTTCTTTTGAGATCACCCCTG---AGAAACCCCAACAGCTTCGGGACTTGA 746
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAAAGAGAGCTTTGATGCTCCACACTTCAACTC 1398
Db 747 TATCTTCTCAGTCTGTGGATATCAACGAGAGCTCTTCTTACACACTTCAATTC 806
QY 1399 AAAGGCCATGGTTATCGTCTGCTCAACAAAGGAACTGGAAACCTTGAACCTGTGGCTGT 1458
Db 807 AAAGGCCATAGTGTACTAGTATTAATGAAGGAGATGCAAAACATTTGAACCTGTGGCAT 866
QY 1459 AAGAAAGACACACACAGAGGGGCGCGGGAAGAGAGGAGGAGCGAAGACGAAGAAGA 1518
Db 867 TAAAGAACCAACACAGAGCAGAAACAGGAAGAGGAACTTTG----- 909
QY 1519 GGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTTTGAAGGAAGGCGATGT 1578
Db 910 -----GAGTGCAAGGTTACAGAGCTGAAATGCTCTGAAGACGATGATT 953
QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGGTTCTCCGAACTCCATCTGCTTG 1638
Db 954 TGTAAATCCAGCAGCTTATCCATTTGTGCTCAACGCTACCTCAACCTCAATTTCTCTGC 1013
QY 1639 CTTTGGTATCAACGCTGAAACAGAACCAACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698
Db 1014 TTTTGGTATCAATGCTGAGAACCAACAGAGGAACTTTCTTGCAGGCGAAGAACAAATGT 1073
QY 1699 GATAGACCATAGAGAGAGCAAGCAAGGAGTATTTAGCAATTCCTGGGTGCGGTGAACAAGT 1758
Db 1074 GGTAAAGCAGATAGAAAGACAACTGACGAGCTTGGTTCCTTGGCTTGCACAGATGT 1133
QY 1759 TGAGAAGCTCATCAAAACACAGAAAGAAATCTCATTTGTGAGTGTGCTGCTCTCA 1812
Db 1134 TGAGAGGCTATTAAAGAGCAGAGGGAATCCTACTTTGTGTGCTCAGCCTCA 1187

RESULT 13
US-10-245-227D-13
; Sequence 13, Application US/10245227D
; Patent No. 6936696
; GENERAL INFORMATION:
; APPLICANT: Monsanto Company
; APPLICANT: Rapp, William D.
; APPLICANT: Peng, Jieixin
; APPLICANT: Nadiq, Gautham
; APPLICANT: Venkatesh, Tyamagondlu
; TITLE OF INVENTION: Enhanced Protein and Methods of Their Use
; FILE REFERENCE: REN-00-087 US
; CURRENT APPLICATION NUMBER: US/10/245, 227D
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: epitope form of beta-conglycinin beta-subunit
US-10-245-227D-13

Query Match 20.0%; Score 406.8; DB 3; Length 1278;
Best Local Similarity 62.1%; Pred. No. 9e-113;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAACCCCTTCTACTT---CCCGTCAAGCGGTTTAGCACCCGCTACGGGAACCAAAA 618
Db 48 GAATAACCCCTTCTACTTTGAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAACCAAAA 107
QY 619 CGGTAGATCCCGGTCTCTCAGAGGTTTGAACAAAGGTCAAGGCAAGTTTCAGAAATCTCCA 678
Db 108 CGGTGCAATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACAACCTTGAGAACCTTCG 167
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QY 679 GAATCACCGTATTGTSCAGATCGAGGCCAAACCTTAACACTCTGTGTTCTTCCCAGCACGC 738
Db 168 AGACTACCCGGATTGTCTCAGTTTCAGTCAAAACCCCAACAACTTCTTCCCACCACATGC 227
QY 739 TGATGCTGATAACATCTCTTGTATCCAGCAAGGGCAAGCCACCGTACCGTAGCAAAATGG 798
Db 228 TGACGCCGATTTCCTCTCTTGTCTTAGCGGGAGCCATACTTACCTTGGTGAACAA 287
QY 799 CAATAACAGAAAGAGCTTTAATCTTGAAGAGGGCCATGCACTCAGAAATCCCATCCGGTTT 858
Db 288 CGACGACAGAGACTCTCTACAACTTCACCTTGCGTAGCCAGAGAAATCCACAGCTGGAAC 347
QY 859 CATTTTCTTACATCTTGAACGGCCATGACAAACAGAACCTTCAGAGTAGCTAAATCTCCAT 918
Db 348 CACTTACTATTGGTTAAACCTTCACGACCAACAGAAATCTCAAAATTAATCAAACTTCCCAT 407
QY 919 GCCCGTTAAACACACACCCGGCCAGTTTGAGGATTTCTTCCGGCGAGCAGCGAGACCAATC 978
Db 408 ACCCGTCAACAAACCTGGCAGATATGATGATTCTTCTTATCTAGCACTCAAGCCCAACA 467
QY 979 ATCTTACTTGCAGGGCTTCAGCAGGAATACGTTTGAAGGGCGCTTCAATGCGGAATTTCAA 1038
Db 468 GTCTACTTGCAGGGCTTCAGCCATAATATTCTAGAGACTCTCTTCCATAGCGAAATTCGA 527
QY 1039 TGAGATACGGAGGTGCTGTTAGNAGAGAAATGCAGAGGTGAGCAAGAGAGAGAGAGGCA 1098
Db 528 GGAGATAAACACAGGGTTTGTGGGAGAGGAAGAGGAGCAGCAGCAAGAG----- 579
QY 1099 GAGGCGATGGAGTACTCGGAGTAGTGAGAAACAATGAAGGAGTGATAGTCAAAAGTGTCAAA 1158
Db 580 -----GGAGTGATCGTGGAACTCTCAAA 602
QY 1159 GGAGCAGCTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 603 GGAACAAATTCGCGAACTGAGCAGACGTCGCCAAATCTAGTTCAAGGAAACCAATTTCTTC 662
QY 1219 AGAGGAGATATCACCAACCCCAATCACTTGAGAGAGGCGCGCGCTTCTTCTTAACAA 1278
Db 663 CGAAGATG-----AACCATTTCACTTGAGAGCGCGAACCCCATCTATTTCCAACAA 713
QY 1279 CTTTGGGAAAGTTATTTGAGGTGAAGCCAGACAGAAAGAACCCCGAGCTTCAGAGCTGGA 1338
Db 714 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCCAACAGCTTCGGGACTTGA 770
QY 1339 CATGATGCTCACTGTGTAGAGATCAAGAAAGAGCTTTGATGCTCCACACTTCAACTC 1398
Db 771 TATCTTCTCAGTCTGTGGATATCAACGAAAGAGCTCTTCTTACCACACTTCAATTC 830
QY 1399 AAAGGCCATGGTTATCGTCTGCTCAACAAAGGAACCTGGAACCTTGAACCTCGTGGCTGT 1458
Db 831 AAAGGCCATAGTATGATAGTATGATGAGAGATGCAACATTTGAACCTTGTGGCAT 890
QY 1459 AAGAAAGAGCAACAAACAGAGGGGACGCGGGGAAGAAAGAGGAGGAGCAAGACGAAGAAGA 1518
Db 891 TAAAGAACCAACACAGAACGAGAAACAGGAAGAGGAACCTTTG----- 933
QY 1519 GGAGGGAAGTAAACAGAGAGCTGCGTAGGTACACAGCGAGGTTTGAAGGAAGGCGATGTT 1578
Db 934 -----GAAAGTCAAGGTACAGAGCTGAAATGCTCTGAAGACGATGATT 977
QY 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTGG 1638
Db 978 TGTAATCCAGCAGCTTATCCATTTGTGCTCAACGCTACCTCAAACTCAATTTCTCTGCG 1037
QY 1639 CTTTGGTATCAACGCTGAAACCAACCAAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698
Db 1038 TTTTGGTATCAATGCTGAGAACCAACAGAGGAACCTTCTTGCAGGCGGAGAAAGACAATGT 1097
QY 1699 GATAGACCATAGAGAGCAAGCAGGAGTATTTAGCAATTCCTGGGTCCGGTGAACAAGT 1758
Db 1098 GGTAAAGCAGATAGAAAGACAAAGTCAGGAGCTTTCGTTCCCTGGGTCTGCACAAGATGT 1157
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Qy 1759 TGAGAGCTCATCAAAACACAGAGGAATCTCACTTTGTGAGTCTCGTCTCA 1812
|||||
Db 1158 TGAGAGGCTATTAAGAGAGAGAGGAATCTCACTTTGTGATGCTCAGCCTCA 1211
|||||

RESULT 14

US-09-108-0108-3
; Sequence 3, Application US/091080108
; Patent No. 6362399
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898

; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,0108
; FILING DATE: 30-Jun-1998

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14, 1996

; ATTORNEY/AGENT INFORMATION:
; NAME: LYNN M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1320 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-108-0108-3

Query Match 20.0%; Score 406.8; DB 3; Length 1320;
Best Local Similarity 62.1%; Pred. No. 9.2e-113;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

Qy 562 GAACAAACCTTCTACTTT---CCGCTCAAGCGGTTTAGCACCGCTACGGGAAACAAA 618
|||
Db 90 GAATACCTTTCTACTTTAGAGCTCTACAGCTTCCAACTCTCTTTGAGAACAAA 149
|||
Qy 619 CGGTAGATCCGGTCTCTGAGAGTTTGAACAAAGTCAAGCGAGTTTCAGAAATCTCCA 678
|||
Db 150 CGTTGCGATTCTCTCCAGAGATTCAACAAACGCTCCCACTTGAAGAACCTTCG 209
|||
Qy 679 GAATACCGTATTCTGAGATCGAGGCAACCTTAACACTTTGTTCTTCCAGCAGCG 738
|||
Db 210 AGACTACCGGATTCTGTCAGTTTCTAGTCAAAACCAACCAACTCTCTCCCCACCATGC 269
|||
Qy 739 TGATGCTGAATACATCTCTGTTATCGAGCAAGGCAAGCCACCGTGACCGTAGCAATGG 798
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Db 270 TGACGGGATTTCTCTCTCTTCTCTTCTAGCGGAGGAGCCATCTACTTCTGTGACAA 329
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Qy 799 CAATAACAGAAAGAGCTTTTAACTTTGACGAGGCGCATGCACTCAGAAATCCCATCCGTTT 858
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RESULT 15

US-09-758-652-3
; Sequence 3, Application US/09758652
; Patent No. 6703544

; GENERAL INFORMATION:

Db 330 CGACGACAGAGACTCTCTACAACTTTCACCTCGCATGCCAGAGAAATCCAGCTGGAAC 389
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Qy 859 CATTTCTTACATCTTGAACCGCATGACACACAGACCTCAGAGTACTTAAATCTCCAT 918
|||
Db 390 CACTTACTATTGGTTAACTTCACTCAGACCAACAGAAATCTCAAAATAATCAAACTTGCAT 449
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Qy 919 GCCGTTTAAACACACCCCGCCAGTTTGAAGATTTCTCCCGCGAGCAGCAGACCAATC 978
|||
Db 450 ACCGTCACAAACCTTGGCAGATATGATGATTTCTTCTATCTAGCACTCAAGCCCAACA 509
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Qy 979 ATCTTACTTGCAGGGCTTTCAGAGGAATAGCTTGGAGCGCGCTTTCAATCGGAATTCAA 1038
|||
Db 510 GTCTTACTTGAAGGGCTTCAAGCCATAATATTTAGAGACCTCTCTTCCATAGCGAATTCGA 569
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Qy 1039 TGAGATACGGAGGGTCTGTTTGAAGAGAAATGCGAGGAGTGAGCAACAGAGAGAGGCA 1098
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Db 570 GGAGATAAACAGGGTTTGTGGAGGAAGAGGAGCAGGAGGCGCAAGAG----- 621
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Qy 1099 GAGCGATGGAGTAGTCTCGGAGTAGTGAGAAATAAGAGGAGTAGTAGTCAAAAGTGTCAA 1158
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Db 622 -----GGAGTGATCTGGAACTCTCAA 644
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Qy 1159 GAGCAGCTTTGAAGAACTTACTAAGCAGCGTAATCGTCTCAAAGAAAGGCTCCGAAGA 1218
|||
Db 645 GGAACAAATTCGGCAACTGAGCAGACGTGCAAAATCTAGTTCAAGGAAACCAATTTCTCTC 704
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Qy 1219 AGAGGGAGATATCACCAACCAATCACTTGAAGAGGCGAGCCCGATCTTTCTTAACA 1278
|||
Db 705 CGAAGATG-----AACCATTTCACTTGAAGCGCCCAACCCCATCTATTTCACAA 755
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Qy 1279 CTTTGGGAAGTTATTTGAGTGAAGCCAGACAGAAAGAACCCCGAGCTTCAGGACCTGGA 1338
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APPLICANT: ANTHONY JOHN KINNEY
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC CLASSES OF SOYBEAN SEED PROTEIN GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNN M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-758-652-3

Query Match 20.0%; Score 406.8; DB 3; Length 1320;
Best Local Similarity 62.1%; Pred.No. 9.2e-113;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAAACCCCTTCTACTT---CCCGTCAAGGCGGTTTAGCACCCGCTACGGGAACCAAAA 618
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DB 150 CGTTCGATTCGCTCTCTCGAGAGTTCAACAAACGCTCCCCAACAACCTTGAGAAACCTCG 209
QY 679 GAATACCCGATTTGTGAGATCGAGGCAAAACCTTAACACTCTTGTCTTCCCAAGCACGC 738
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Search completed: June 23, 2006, 10:41:41
Job time : 326.712 secs


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Db 1981 CTACTATCAAAACCTTATCAATAAATAAAGCTTTGTCGTTGTTCTCC 2032
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RESULT 2

US-10-228-806-1

; Sequence 1, Application US/10228806

; Publication No. US20030049237A1

; GENERAL INFORMATION:

; APPLICANT: Bannan, et al.

; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions

; TITLE OF INVENTION: to Allergy

; FILE REFERENCE: 2002834-0043

; CURRENT APPLICATION NUMBER: US/10/228,806

; CURRENT FILING DATE: 2002-08-26

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2032

; TYPE: DNA

; ORGANISM: Arachis hypogaea

US-10-228-806-1

Query Match 100.0%; Score 2032; DB 6; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1981 CTACTATCAAAACCTTATCAATAAAACGTTTGTGCGTTGTTCTCC 2032

RESULT 3

US-10-100-303A-5
; Sequence 5, Application US/10100303A
; Publication No. US20030202980A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0166
; CURRENT APPLICATION NUMBER: US/10/100,303A
; CURRENT FILING DATE: 2002-03-18

[illegible]

Db 1981 CTAATATCCAAAACTTATCAATAAATAAAAAAGTTTGTGCGTTGTTCTCC 2032

RESULT 4

US-10-728-323-1

; Sequence 1, Application US/10728323

; Publication No. US2004020894A1

; GENERAL INFORMATION:

; APPLICANT: Caplan, Michael J.

; APPLICANT: Bottomly H., Kim

; APPLICANT: Sosin B., Howard

; APPLICANT: Burks A., Wesley

; APPLICANT: Sampson A., Hugh

; TITLE OF INVENTION: Microbial Delivery System

; FILE REFERENCE: 2002834-0232

; CURRENT APPLICATION NUMBER: US/10728,323

; CURRENT FILING DATE: 2003-12-04

; PRIOR APPLICATION NUMBER: 60/195,035

; PRIOR FILING DATE: 2000-04-06

; PRIOR APPLICATION NUMBER: 09/731,375

; PRIOR FILING DATE: 2000-12-06

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2032

; TYPE: DNA

; ORGANISM: Arachis hypogaea

US-10-728-323-1

Query Match 100.0%; Score 2032; DB 9; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1381 GCTCCCACTTTCAACTCAAAGGCCATGTTTATCGTCTGCTCAACAAAGAGAACTGGAAA 1440
QY 1441 CTTTGAATCTGCTGCTGTAAGAAAGAGCAACAGAGAGGAGCGGCGGAAGAGAGGA 1500
Db 1441 CTTTGAATCTGCTGCTGTAAGAAAGAGCAACAGAGAGGAGCGGCGGAAGAGAGGA 1500
QY 1501 GGAAG 1560
Db 1501 GGAAG 1560
QY 1561 GAAG 1620
Db 1561 GAAG 1620
QY 1621 CGAATCTTCACTTGTGCTTCCGATCAACCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 CGAATCTTCACTTGTGCTTCCGATCAACCGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1681 AGGTGATAGGAGCAATGTGATAGACGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740

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Db 1681 AGGTGATAGGACAAATGTGATAGACAGATAGAGAAAGCAAGCGAAGATTTAGCATTTCC 1740
Qy 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCGAAGGAATCTCAGTTGTGAG 1800
Db 1741 TGGGTCGGGTGAACAAGTTGAGAAGCTCATCAAAAACCGAAGGAATCTCAGTTGTGAG 1800
Qy 1801 TGGTCTGCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCGAGAA 1860
Db 1801 TGGTCTGCTCAATCTCAATCTCAATCTCGTCTCTCTGAGAAAGAGTCTCTCGAGAA 1860
Qy 1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGAAGGTCACCTCTTCAATTTTGAAGGC 1920
Db 1861 AGAGGATCAAGAGGAGGAAACCAAGGAGGAAGGTCACCTCTTCAATTTTGAAGGC 1920
Qy 1921 TTTTAACTGAGAATGGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT 1980
Db 1921 TTTTAACTGAGAATGGAGGCAACTTGTATGATCGATAATAAGATCAAGCTTTTGTACT 1980
Qy 1981 CTACTATCCAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032
Db 1981 CTACTATCCAAAACCTTATCAATAAATAAAAACGTTTGTGCGTTGTTCTCC 2032

RESULT 5
US-10-728-051-1
; Sequence 1, Application US/10728051
; Publication No. US20040234548A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002634-0222
; CURRENT APPLICATION NUMBER: US/10/728,051
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-051-1

Query Match 100.0%; Score 2032; DB 9; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
Db 1 AATAATCATATATATTCATCAATCATCTATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
Qy 61 GGTTCCTCCACTGATGCTGTGTGCTAGGGATCCTTGCTCGGCTTCAGTTTCTGCAACGCA 120
Db 61 GGTTCCTCCACTGATGCTGTGTGCTAGGGATCCTTGCTCGGCTTCAGTTTCTGCAACGCA 120
Qy 121 TGCCAAGTCAATCACTTACAGAGAAACCAAGAGAACCCCTGCGCCAGAGGTCCTCCA 180
Db 121 TGCCAAGTCAATCACTTACAGAGAAACCAAGAGAACCCCTGCGCCAGAGGTCCTCCA 180
Qy 181 GAGTTGTCAACAGNACCGGATGACTTTGAAGCAAAAGGCGATCGAGTCTCGTGCACCA 240
Db 181 GAGTTGTCAACAGNACCGGATGACTTTGAAGCAAAAGGCGATCGAGTCTCGTGCACCA 240
Qy 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACATCGGCAACCAACCA 300
Db 241 GCTCGAGTATGATCCTCGTTGTGTCTATGATCCTCGAGGACACATCGGCAACCAACCA 300
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Qy 301 AGCTTCCCCTCAGGGAGGGACAGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360
Db 301 AGCTTCCCCTCAGGGAGGGACAGTGGCCGCCAACCCGGAGACTACGATGATGACCG 360
Qy 361 CCGTCAACCCCGAAGAGAGAGGAGCGCGATGGGACACAGCTGGACCCAGCGAGGAGGTGA 420
Db 361 CCGTCAACCCCGAAGAGAGAGGAGCGCGATGGGACACAGCTGGACCCAGCGAGGAGGTGA 420
Qy 421 AAGAGAAGAGACTTGGAGACACCAAGAGAAGATTGGAGGCGACCAAGTCATCAGCAGCC 480
Db 421 AAGAGAAGAGACTTGGAGACACCAAGAGAAGATTGGAGGCGACCAAGTCATCAGCAGCC 480
Qy 481 ACGGAAATAAGCCCCGGAAGGAGAGCAAGSAGAACAAAGAGTGGGGAACACACAGGTAGCCA 540
Db 481 ACGGAAATAAGCCCCGGAAGGAGAGAGCAAGAGAGAACAAAGAGTGGGGAACACACAGGTAGCCA 540
Qy 541 TGTGAGGGGAAGAAACATCTCGGAACAAACCTTTTCTACTTTCCCGTCAAGGCGTTTAGCAC 600
Db 541 TGTGAGGGGAAGAAACATCTCGGAACAAACCTTTTCTACTTTCCCGTCAAGGCGTTTAGCAC 600
Qy 601 CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCCTGCAGAGGTTTGACCAAAAGGTCAAG 660
Db 601 CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCCTGCAGAGGTTTGACCAAAAGGTCAAG 660
Qy 661 GCAGTTTTCAGAACTCTCCAGAAATCACCGTATTTGTGCAGATCGAGGCCAAACCTTAACACTCT 720
Db 661 GCAGTTTTCAGAACTCTCCAGAAATCACCGTATTTGTGCAGATCGAGGCCAAACCTTAACACTCT 720
Qy 721 TGTTCCTTCCCAAGCACGCTGATGATAACATCTTGTATCCAGCAAGGGAAGCCAC 780
Db 721 TGTTCCTTCCCAAGCACGCTGATGATAACATCTTGTATCCAGCAAGGGAAGCCAC 780
Qy 781 CGTGACCGTAGCAAAATGGCAATTAAGAAAGAGCTTTAATCTTTCAGAGGCGCATGCAC 840
Db 781 CGTGACCGTAGCAAAATGGCAATTAAGAAAGAGCTTTAATCTTTCAGAGGCGCATGCAC 840
Qy 841 CAGAATCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCATGACAAACAGAACCTCAG 900
Db 841 CAGAATCCCATCCGGTTTCATTTCTTACATCTTTGAACCGCATGACAAACAGAACCTCAG 900
Qy 901 AGTAGCTAAATCTCCATGCCCGTTAAACACACCCGCCAGTTTTCAGGATTTTTCGCGGC 960
Db 901 AGTAGCTAAATCTCCATGCCCGTTAAACACACCCGCCAGTTTTCAGGATTTTTCGCGGC 960
Qy 961 GAGCAGCCGAGACCAATCATCTTCTTTCAGGGCTTCAGCAGGAATACGTTGGAGCGGC 1020
Db 961 GAGCAGCCGAGACCAATCATCTTCTTTCAGGGCTTCAGCAGGAATACGTTGGAGCGGC 1020
Qy 1021 CTTCAATCGGAATTCAAATGAGATACGAGGGTGCTTTAGAAAGAAATCGAGAGGTGA 1080
Db 1021 CTTCAATCGGAATTCAAATGAGATACGAGGGTGCTTTAGAAAGAAATCGAGAGGTGA 1080
Qy 1081 GCAAGAGGAGAGAGGCGAGAGGCGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140
Db 1081 GCAAGAGGAGAGAGGCGAGAGGCGATGGAGTACTCGGAGTAGTGAGAACAAATGAAGAGT 1140
Qy 1141 GATAGTCAAGTGTCAAAGGAGCACGTTGAGAACTTACTTAAGCACGCTAAATCCGCTCTC 1200
Db 1141 GATAGTCAAGTGTCAAAGGAGCACGTTGAGAACTTACTTAAGCACGCTAAATCCGCTCTC 1200
Qy 1201 AAAGAAAGGCTCCGAAGAGAGAGGAGATATCACCAACCCCAATCACTTGAGAGAAGCGCA 1260
Db 1201 AAAGAAAGGCTCCGAAGAGAGAGGAGATATCACCAACCCCAATCACTTGAGAGAAGCGCA 1260
Qy 1261 GCCCGATCTTTCTAAACAACTTTTCGGGAAGTTATTGAGGTGAAGCCAGACAAGAGAACC 1320
Db 1261 GCCCGATCTTTCTAAACAACTTTTCGGGAAGTTATTGAGGTGAAGCCAGACAAGAGAACC 1320
Qy 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGATAGATCAAAAGAGAGCTTTGAT 1380
Db 1321 CCAGCTTCAGGACCTGGACATGATGCTCACCTGTGATAGATCAAAAGAGAGCTTTGAT 1380
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QY 1141 GATAGTCAAGTGTCAAAGGAGCAGCTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTC 1200
Db 1141 GATAGTCAAGTGTCAAAGGAGCAGCTTGAAGAACTTACTAAGCAGCGTAAATCCGTCTC 1200
QY 1201 AAAGAAGGCTCCGAAGAAGAGGAGATATCAACCAACCAATCACTTGAAGAGGCGCA 1260
Db 1201 AAAGAAGGCTCCGAAGAAGAGGAGATATCAACCAACCAATCACTTGAAGAGGCGCA 1260
QY 1261 GCCCGATCTTTCTAACAACCTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
Db 1261 GCCCGATCTTTCTAACAACCTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAACCC 1320
QY 1321 CAGCTTCAGGACCTGGACATGATGTCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
Db 1321 CAGCTTCAGGACCTGGACATGATGTCTACCTGTGTAGAGATCAAAAGAGGAGCTTTGAT 1380
QY 1381 GCTCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCAACAAAGGAACTCGAAA 1440
Db 1381 GCTCCACACTTCAACTCAAAGGCCATGGTTATCGTCGTCAACAAAGGAACTCGAAA 1440
QY 1441 CTTGAACTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAAAGAGGA 1500
Db 1441 CTTGAACTCGTGGCTGTAAAGAAAGAGCAACACAGAGGGGACGCGGGAAGAAAGAGGA 1500
QY 1501 GGAAGAGGAGGAGGAGGAGGAGTAAACAGAGAGGTGCGTAGTACACAGCGAGGTT 1560
Db 1501 GGAAGAGGAGGAGGAGGAGGAGTAAACAGAGAGGTGCGTAGTACACAGCGAGGTT 1560
QY 1561 GAAGGAGGAGGAGTGTTCATCATGTCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTC 1620
Db 1561 GAAGGAGGAGGAGTGTTCATCATGTCAGCAGCTCATCCAGTAGCCATCAACGCTTCCTC 1620
QY 1621 CGAACTCCATCTCGTTCGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCCTTC 1680
Db 1621 CGAACTCCATCTCGTTCGGCTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCCTTC 1680
QY 1681 AGTGATAGGACAAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTTAGCATTCCTCC 1740
Db 1681 AGTGATAGGACAAATGTGTATAGACAGATAGAGAGCAAGCAAGGATTTAGCATTCCTCC 1740
QY 1741 TGCGTGGGTGAACAAGTTCAGAGGCTCATCAAAAACCAAGAGAAATCTCACCTTGTGAG 1800
Db 1741 TGCGTGGGTGAACAAGTTCAGAGGCTCATCAAAAACCAAGAGAAATCTCACCTTGTGAG 1800
QY 1801 TGCTCGTCTCAATCTCAATCTCGCTCTCGCTCTCTCTGAGAAAGAGTCTCTCGAGAA 1860
Db 1801 TGCTCGTCTCAATCTCAATCTCGCTCTCGCTCTCTCTGAGAAAGAGTCTCTCGAGAA 1860
QY 1861 AGAGGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Db 1861 AGAGGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
QY 1921 TTTTAACTGAGATGGAGGCAACTTGTATGTATCGATAAAGATCAAGCTTTTGTACT 1980
Db 1921 TTTTAACTGAGATGGAGGCAACTTGTATGTATCGATAAAGATCAAGCTTTTGTACT 1980
QY 1981 CTACTATCCAAAACTTATCAATAAATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2032
Db 1981 CTACTATCCAAAACTTATCAATAAATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2032
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RESULT 7
US-10-958-324-5
; Sequence 5, Application US/10958324
; Publication No. US20050114924A1
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; TRANSGENIC PEANUT SEEDS
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; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/10/958,324
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2032
; TYPE: DNA
; ORGANISM: Arachis hypogaea
; US-10-958-324-5

Query Match 100.0%; Score 2032; DB 10; Length 2032;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATAATCATATATATTCATCAATCATATATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
Db 1 AATAATCATATATATTCATCAATCATATATATAGTAGTAGCAGGAGCAATGAGAGGAG 60
QY 61 GGTTCCTCCACTGATGCTGTGCTAGGGATCCTTGTCTCTGGTTCAGTTTCTGCAACGCA 120
Db 61 GGTTCCTCCACTGATGCTGTGCTAGGGATCCTTGTCTCTGGTTCAGTTTCTGCAACGCA 120
QY 121 TGCCAAAGTCAATCACTTACAGAAAGAAACAGAGAAACCCCTGCGCCAGAGGTTGCTTCCA 180
Db 121 TGCCAAAGTCAATCACTTACAGAAAGAAACAGAGAAACCCCTGCGCCAGAGGTTGCTTCCA 180
QY 181 GAGTTGTCACAGGAAACCGGATGACTTGAAGCAAAAGGATCGAGTCTCGCTGCAACCA 240
Db 181 GAGTTGTCACAGGAAACCGGATGACTTGAAGCAAAAGGATCGAGTCTCGCTGCAACCA 240
QY 241 GCTCGAGTATGATCCTCGTGTGTATGATCTCTGAGGACACACTTGGCAACCAACCA 300
Db 241 GCTCGAGTATGATCCTCGTGTGTATGATCTCTGAGGACACACTTGGCAACCAACCA 300
QY 301 AGTTTCCCTCCAGGGGAGCGGACACGTCGGCGCCAAACCGGAGACTAGATGATGACCG 360
Db 301 AGTTTCCCTCCAGGGGAGCGGACACGTCGGCGCCAAACCGGAGACTAGATGATGACCG 360
QY 361 CGCTCAACCCCGAAGAGAGAGGAGGCGCGATGGGGACCACTGGACCGAGGAGGCTGA 420
Db 361 CGCTCAACCCCGAAGAGAGAGGAGGCGCGATGGGGACCACTGGACCGAGGAGGCTGA 420
QY 421 AAGAGAAGAAAGACTGAGAGCAACCAAGAGAAGATTGGAGGCGCACCAAGTCTATCAGAGCC 480
Db 421 AAGAGAAGAAAGACTGAGAGCAACCAAGAGAAGATTGGAGGCGCACCAAGTCTATCAGAGCC 480
QY 481 ACGGAAAATAAGGCCCGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 ACGGAAAATAAGGCCCGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TGTGAGGAGAGAGAAACATCTCGGAACAACTTTCTACTTCCCGTCAAGGCGGTTTAGCAC 600
Db 541 TGTGAGGAGAGAGAAACATCTCGGAACAACTTTCTACTTCCCGTCAAGGCGGTTTAGCAC 600
QY 601 CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCTTGCAAGAGTTTGAACCAAGGTTCAAG 660
Db 601 CCGCTACGGGAACCAAAACCGTAGGATCCGGGTCTTGCAAGAGTTTGAACCAAGGTTCAAG 660
QY 661 GCAGTTTCAGAAATCTCAGAAATCACCCTGATTTGTCAGATCGAGGCGCAAACTAACACTCT 720
Db 661 GCAGTTTCAGAAATCTCAGAAATCACCCTGATTTGTCAGATCGAGGCGCAAACTAACACTCT 720
QY 721 TGTTCCTTCCCAAGCAGCTGATGCTGATTAACATCTTGTATCCAGCAAGGAGGAGCCAC 780
Db 721 TGTTCCTTCCCAAGCAGCTGATGCTGATTAACATCTTGTATCCAGCAAGGAGGAGCCAC 780
QY 781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTGACGAGGCGCATGCACT 840
Db 781 CGTGACCGTAGCAAAATGGCAATTAACAGAAAGAGCTTTAATCTTTGACGAGGCGCATGCACT 840
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781	Db	CGTGACCGTGTAGCAAAATGCGCAATTAACAGAAAGAGCTTTAAATCTTTGAACGAGGGCCATGCAC	840
841	Qy	CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTTGAAACCGGCATACACAACACAGAAACCTCAG	900
841	Db	CAGAAATCCCATCCGGTTTCAATTTCTTACATCTTTGAAACCGGCATACACAACACAGAAACCTCAG	900
901	Qy	AGTAGCTTAAATCTCATGCGCGGTAAACACACCGCGCCAGTTTGAAGATTTCTTCCGGC	960
901	Db	AGTAGCTTAAATCTCCAATGCGCGGTAAACACACCGCGCCAGTTTGAAGATTTCTTCCGGC	960
961	Qy	GAGCAGCCGAGACCAATCATCTTACTTTGACGGCTTCAGCAGGAATACGTTGTGAGGCGCG	1020
961	Db	GAGCAGCCGAGACCAATCATCTTACTTTGACGGCTTCAGCAGGAATACGTTGTGAGGCGCG	1020
1021	Qy	CTTTCAATSCGGAAATTCATAGATACGCGAGGGTCTGTTAGAAAGAAATACGAGGAGTGA	1080
1021	Db	CTTTCAATSCGGAAATTCATAGATACGCGAGGGTCTGTTAGAAAGAAATACGAGGAGTGA	1080
1081	Qy	GCAAGAGGAGAGGGCAGAGCGATCGAGTACTCGAGTAGTGAGNAACAATGAAGAGT	1140
1081	Db	GCAAGAGGAGAGGGCAGAGCGATCGAGTACTCGAGTAGTGAGNAACAATGAAGAGT	1140
1141	Qy	GATAGTCAAAAGTGTCAAAAGGACGCTTGAGAACTTACTAAGCAGCTAAATCCCGTCTC	1200
1141	Db	GATAGTCAAAAGTGTCAAAAGGACGCTTGAGAACTTACTAAGCAGCTAAATCCCGTCTC	1200
1201	Qy	AAAGAAAGGCTCCGAAGAGAGGGAGATATCACCAACCCCAATCAACTTGAGAGAAAGCGGA	1260
1201	Db	AAAGAAAGGCTCCGAAGAGAGGGAGATATCACCAACCCCAATCAACTTGAGAGAAAGCGGA	1260
1261	Qy	GCCCGATCTTTTAAACAATTTGGGAAGTTATTGTGAGGTGAAGCCAGACAGAAAGAACCC	1320
1261	Db	GCCCGATCTTTTAAACAATTTGGGAAGTTATTGTGAGGTGAAGCCAGACAGAAAGAACCC	1320
1321	Qy	CCAGCTTCAGGACCTGACATGATGCTCACTGTGTAGAGATCAAGAGAGGAGCTTTGAT	1380
1321	Db	CCAGCTTCAGGACCTGACATGATGCTCACTGTGTAGAGATCAAGAGAGGAGCTTTGAT	1380
1381	Qy	GCTCCCCACATTCAACTCAAAGGCCATGGTTATCGTCTGCTCAAACAAAGGAATCTGAAA	1440
1381	Db	GCTCCCCACATTCAACTCAAAGGCCATGGTTATCGTCTGCTCAAACAAAGGAATCTGAAA	1440
1441	Qy	CCTTGAACTCGTGGCTGTAAAGAAAGACCAACACAGAGGGGACGGCGGGAAGAAAGGA	1500
1441	Db	CCTTGAACTCGTGGCTGTAAAGAAAGACCAACACAGAGGGGACGGCGGGAAGAAAGGA	1500
1501	Qy	GGAGGAAGACGAAGAGAGAGGGAAGTAAACAGAGAGTCCGTAGGTACACACGGAGTT	1560
1501	Db	GGAGGAAGACGAAGAGAGAGGGAAGTAAACAGAGAGTCCGTAGGTACACACGGAGTT	1560
1561	Qy	GAAGGAAGGCGATGTTGTTCAATCATGCCAGCAGCTCATCCAGTAGTACCATCAACGCTTCCTC	1620
1561	Db	GAAGGAAGGCGATGTTGTTCAATCATGCCAGCAGCTCATCCAGTAGTACCATCAACGCTTCCTC	1620
1621	Qy	CGAATCCATCTGCTTGGCTTCGGTATCAACGCTGAAAAACCAACACAGAAATCTTCCTTGC	1680
1621	Db	CGAATCCATCTGCTTGGCTTCGGTATCAACGCTGAAAAACCAACACAGAAATCTTCCTTGC	1680
1681	Qy	AGGTGATAAGGACAAATGTGTATAGACACAGATAGAGAACGAAGGATTTAGCATTC	1740
1681	Db	AGGTGATAAGGACAAATGTGTATAGACACAGATAGAGAACGAAGGATTTAGCATTC	1740
1741	Qy	TGGGTCCGGGTGAAACAGTTGAGAGCTCATCAAAACCAAGAGAAATCTCACATTTGTGAG	1800
1741	Db	TGGGTCCGGGTGAAACAGTTGAGAGCTCATCAAAACCAAGAGAAATCTCACATTTGTGAG	1800
1801	Qy	TGCTCGTCTCAATCTCAATCTCAATCTCGCTCGTCTCCTGAGAAAGAGTCTCCTCAGAA	1860
1801	Db	TGCTCGTCTCAATCTCAATCTCAATCTCGTCTCCTGAGAAAGAGTCTCCTCAGAA	1860
1861	Qy	AGAGGATCAAGAGGAGGAAAAACCAAGAGGGGAAGGGTCTCACTCTTTCAATTTTGAAGGC	1920
1861	Db	AGAGGATCAAGAGGAGGAAAAACCAAGAGGGGAAGGGTCTCACTCTTTCAATTTTGAAGGC	1920

[illegible]

RESULT 8

US-10-100-303A-6 ; Sequence 6, Application US/10100303A
; Publication No. US20030202980A1

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; GENERAL INFORMATION:
; APPLICANT: Caplan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002B34-0166
; CURRENT APPLICATION NUMBER: US/100,303A
; CURRENT FILING DATE: 2002-03-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1949
; TYPE: DNA
; ORGANISM: Arachis hypogaea, Prot/Nucleo-Ara h 1
US-10-100-303A-6

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	Query Match	86.2%	Score 1752.4;	DB 7;	Length 1949;
	Best Local Similarity	95.0%;	Pred. No. 0;		
	Matches 1894; Conservative	0;	Mismatches 46;	Indels 54;	Gaps 6;
Qy	48	CAATGAGAGGGGGTTTCTCCACTGATGCTGTGTCTAGGGATCCTTGTCCTGGCTTCAG	107		
Dd	1	CAATGAGAGGGAGGGTTTCTCCACTGAATGCTGTGTGGGATCCCTTGTCCTGGCTTCAG	60		

QY 648 ACCAAAGGTCAAGCGAGTTTCAGAACTCCAGAAATCACGTAATTGTGCAGATCGAGGCCA 707
Db |||||
QY 583 ACCAAAGGTCAAGCGAGTTTCAGAACTCCAGAAATCACGTAATTGTGCAGATCGAGGCCA 642
Db |||||
QY 708 AACCTAACACTCTTGTCTTCCCAAGCAGCGTGAATACATCCTTGTATCCAGC 767
Db |||||
QY 643 GACCTAACACTCTTGTCTTCCCAAGCAGCGTGAATACATCCTTGTATCCAGC 702
QY 768 AAGGGCAAGCCACCGTAGCGTAGCAAAATGGGAATTAACAGAAAGAGCTTTAATCTTGACG 827
Db |||||
QY 703 AAGGCAAGCCACCGTAGCGTAGCAAAATGGGAATTAACAGAAAGAGCTTTAATCTTGACG 762
QY 828 AGGGCCATGCACTCAGAACTCCCATCCGTTTCAATCTTCTACATCTTTGAACCGGCATGACA 887
Db |||||
QY 763 AGGGCCATGCACTCAGAACTCCCATCCGTTTCAATCTTCTACATCTTTGAATCGACATGACA 822
QY 888 ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGCCAGTTTGAGG 947
Db |||||
QY 823 ACCAGAACCTCAGAGTAGCTTAAATCTCCATGCCGTTTAAACACACCCGCCAGTTTGAGG 882
QY 948 ATTTCTTCCGGCGAGAGCGGAGACCAATCATCTTCTGAGGCGTTCAGCAGGAATA 1007
Db |||||
QY 883 ATTTCTTCCGGCGAGAGCGGAGACCAATCATCTTCTGAGGCGTTCAGCAGGAATA 942
QY 1008 CGTTGGAGCGCGCTTCAATGCCGAATTCGAATCAGATACGAGGGTCTGTAGAGAGA 1067
Db |||||
QY 943 CTTTGGAGCGCGCTTCAATGCCGAATTCGAATCAGATACGAGGGTCTGTAGAGAGA 1002
QY 1068 ATGCAGGAGGTGAGCAAGAGAGAGAGGCGAGAGCGATGGAGTACTCGGAGTAGTGAGA 1127
Db |||||
QY 1003 ATGCAGGAGAGCAAGAGAGAGAGGCGAGAGCGAGAGTACTCGGAGTAGTG--- 1059
QY 1128 ACAATGAAGAGGTAGTAGTCAAAAGTGTCAAGAGACAGCTTGAAGAACTTACTAAGCACG 1187
Db |||||
QY 1060 ATAATGAAGAGGTAGTAGTCAAAAGTGTCAAGAGAGCAGCTTCAAGAACTTACTAAGCACG 1119
QY 1188 CTAATTCGGTCTCAAGAGAGGCTCCGAGAGAGGAGATACCAACCCCAATCAACT 1247
Db |||||
QY 1120 CTAATTCGGTCTCAAGAGAGGCTCC---GAAGAGGAAGATATCAACACCCCAATCAACT 1176
QY 1248 TGAGAGAGGCGAGCCCGATCTTTTAAACAACCTTTGGGAAGTTATTGTAGGTGAAGCCAG 1307
Db |||||
QY 1177 TGAGAGATGCGAGCCCGATCTTTTAAACAACCTTTGGGAGTTATTGTAGGTGAAGCCAG 1236
QY 1308 ACAAGAGAAACCCCGAGCTTCAGGACCTGGAATGATGCTCACTGTGTAGAGATCAAAG 1367
Db |||||
QY 1237 ACAAGAGAAACCCCGAGCTTCAGGACCTGGACATGATGCTCACTGTGTAGAGATCAAAG 1296
QY 1368 AAGGAGCTTTGATGCTCCACACTTCAACTCAAGGCCATGGTTATCGTCTCAACA 1427
Db |||||
QY 1297 AAGGAGCTTTGATGCTCCACACTTCAACTCAAGGCCATGGTATCGTCTCAACA 1356
QY 1428 AAGGAACCTTGAAACCTTGAACTCGTGGCTGTGAAGAAAGAGCAACACAGAGGGGCGGC 1487
Db |||||
QY 1357 AAGGAACCTTGAAACCTTGAACTCGTGGCTGTGAAGAAAGAGCAACACAGAGGGGCGGC 1416
QY 1488 GGGAA-----GAAGAGGAGGACGAGACGAGAGAGAGGAGGAATTAACAGAGAGG 1538
Db |||||
QY 1417 GGGAAACAGAGTGGGAGAGAGAGGAGAGATGAAGAGAGGAGGGAAGTAAACAGAGAGG 1476
QY 1539 TGCGTAGGTACAGCGAGGTTGAAGGAGGCGATGTGTTCATCATGCCAGCAGCTCATC 1598
Db |||||
QY 1477 TGCGTAGGTACAGCGAGGTTGAAGGAGGCGATGTGTTCATCATGCCAGCAGCTCATC 1536
QY 1599 CAGTAGCATCAACCGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACCGCTGAAA 1658
Db |||||
QY 1537 CAGTAGCATCAACCGCTTCTCCGAACTCCATCTGCTTGGCTTCGGTATCAACCGCTGAAA 1596
QY 1659 ACAACACAGAAATCTTCTTGCAGGTGATGAAGACATGTGATAGACCATGAGAGG 1718
Db |||||
QY 1597 ACAACACAGAAATCTTCTTGCAGGTGATGAAGACATGTGATAGACCATGAGAGG 1656
QY 1719 AAGCGAAGGATTTAGCATTCCTCGGGTGAACAAGTTGAGAGCTCATCAAAAACC 1778

Db 1657 AAGCGAAGATTTAGCATTCCTCGTTCCGGTGAACAAGTTGAGAAGCTCATCAAAAACC 1716
QY 1779 AGAAGAAATCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCGTCTCTC 1838
Db |||||
QY 1717 AGAGGAGTCTCACTTTGTGAGTGTCTGCTCAATCTCAATCTCAATCTCGTCTC----- 1765
QY 1839 CTGAGAAAGAGTCTCTCTGAGAAAGAGGATCAAGAGGAGGAGAAACCAAGAGGAGGAGGTC 1898
Db |||||
QY 1766 -----GTCTCTCTGAAAAGAGGATCAAGAGGAGGAGAAACCAAGAGGAGGAGGTC 1815
QY 1899 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGCAACTTGTATGTATCGAT 1958
Db |||||
QY 1816 CACTCTCTTCAATTTTGAAGGCTTTTAACTGAGAATGGAGGAACTTGTATGTATCCAT 1875
QY 1959 AATAAGATCACGCTTTTGTACTCTACTATCCAAAACCTTATCAATAAATAAAACGTTTG 2018
Db |||||
QY 1876 AATAAGATCACGCTTTTGTAACTACTATCCAAAACCTTATCAATAAATAAAACGTTTG 1935
QY 2019 TCGGTTGTTTCTCC 2032
Db |||||
QY 1936 TCGGTTGTTTCTCC 1949

RESULT 9
US-10-245-227B-15
; Sequence 15, Application US/10245227B
; Publication No. US20030200558A1
; GENERAL INFORMATION:
; APPLICANT: Peng, JieXin
; APPLICANT: Rapp, William
; APPLICANT: Nadig, Gautham
; APPLICANT: Venkatesh, T
; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE
; FILE REFERENCE: REN-00-087-US
; CURRENT APPLICATION NUMBER: US/10/245,227B
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mature form of beta-conglycinin beta-subunit
US-10-245-227B-15

Query Match 20.0%; Score 406.8; DB 7; Length 1254;
Best Local Similarity 62.1%; Pred. No. 4.2e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAAACCTTTCTACTT---CCCGTCAAGGCGGTTTAGCACCCGCTACGGNACCAAAA 618
Db |||||
QY 619 CGGTAGGATCCGGTCTCGCAGAGGTTTCACAAAGGTCAAGSCAGTTTCAGAAATCTCCA 678
Db |||||
QY 84 CGGTGCATTCGTCTCTCCAGAGATTCAACAAAACGCTCCCAACAACCTTTGAGAACCTTCG 143
QY 679 GAATCACCGTATTGTGCAGATCGAGGCCAAAACCTTAACACTCTTGTTCCTTCCCAAGCAGC 738
Db |||||
QY 144 AGACTACCGGATTTGTCAGTTTCAGTCAAAAACCAACAACAATCTTCTCCCAACCATGC 203
QY 739 TGATGCTGATAATCATCTTGTGTTATCCAGCAAGGCAAGCACCCTGACCGTAGCAATGG 798
Db |||||
QY 204 TGACGCCGATTTCTCTCTCTTTGTCCTTAGCGGAGAGCCATACCTTACCTTGGTGAACAA 263
QY 799 CAATAACAGAAAGAGCTTTTAACTTTGACGAGGCGCCATGCACCTCAGAAATCCCATCCCGTTT 858
Db |||||
QY 264 CGACGACAGAGACTCTCTACAACTTCCAGTATGCCAGAGATCCAGCTGGAAC 323
QY 859 CATTTCTCATCTTTGAACCGGCATGACAAACCGCATGACAACTCAGAGTAGCTTAAATCTCCAT 918
Db |||||

Db 324 CACTTACTATTTGGTTAAACCTCAGACCCAGAAATCTCAAAATAATCAAACTTGGCAT 383
Qy 919 GCCGGTTAAACACACCCCGCCAGTTTGAGGATTTCTCCCGCGAGCAGCCGAGACCAATC 978
Db 384 ACCGTCACAAACCTGGCAGATATGATTTCTTATCTAGCACTCAAGCCCAACA 443
Qy 979 ATCTTACTTTCAGGGCTTTCAGCAGGAATACTGTTGGAGCGCCCTTCAATCGGAATTCAA 1038
Db 444 GTCTTACTTTCAGGGCTTTCAGCCATAATTTCTAGAGACCTCTCTCCATAGCGAATTCGA 503
Qy 1039 TGAGATACGAGGGTCTGTTTAGAAGAAATGTCAGGAGGTGAGCAAGAGGAGAGGGCA 1098
Db 504 GGAGATAACAGGGTCTGTTTGGAGAGGAAGAGGAGCAGGAGGCAAG----- 555
Qy 1099 GAGGCGATGAGTACTCGGAGTAGTGAGAACATGAAGGAGTGTAGTCAAAAGTGTCAAA 1158
Db 556 -----GGAGTGATCTGGAACTCTCAAA 578
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCTTAATTCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 579 GGAACAAATTCGGCAACTGAGCAGACGTGCCAAATCTAGTTCAAGGAAACCAATTTCTC 638
Qy 1219 AGAGGAGATATCACCAACCAATCAACTTTCAGAGAGGCGAGCCGATCTTTCTAACAA 1278
Db 639 CGAAGATG-----AACCATTTCAACTTGAAGAGCCGCAACCCCATCTATTCCAAACA 689
Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAAGAACCCCGAGCTTCAGGACCTGGA 1338
Db 690 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCCAACAGCTTCGGAGCTTGA 746
Qy 1339 CATGATGCTCACCTGTGTAGAGATCAAGAAAGGAGCTTTGATGCTCCCACTTCAACTC 1398
Db 747 TATCTCTCTCAGTCTGTGATATCAACGAAGGAGCTCTTTCTTACCACTTCAATTC 806
Qy 1399 AAAGGCCATGGTATCTGCTGCTCAACAAAGNACTGGAAACCTTGAACCTGCGCTGT 1458
Db 807 AAAGGCCATAGTATAGTATGATTAATGAAGGAGATGCAAAATTTGAACCTTGTGGCAT 866
Qy 1459 AAGAAAGAGCAACACAGAGGGGAGCGCGGGAAGAGAGGAGGACGAAGACGAAGAAGA 1518
Db 867 TAAAGAACACACAGAGAGCAAGAAACAGGAAGGAACCTTTG----- 909
Qy 1519 GGAGGGAAGTAACAGAGAGGTGCTAGGTACACAGCGAGGTTGAAGAGCGGATGTGT 1578
Db 910 -----GAAGTGCAGAAAGGTACAGAGCTGAAATTTCTGAAGACGATGTATT 953
Qy 1579 CATATGCGAGAGCTCATCCAGTAGCCATCAAGCTTCTCCGAACCTCATCTGCTTGG 1638
Db 954 TGTAAATTCAGAGCTTATCTCATTTGTGTCAGCGCTACCTCAAACTCAATTTCTCTGC 1013
Qy 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAACTCTTCTTCAGGTGATAGGCAATGT 1698
Db 1014 TTTTGGTATCAATGCTGAGAAACACAGAGAACTTCTTTCAGGCGAGAAAGCAATGT 1073
Qy 1699 GATAGACCATAGAGAAAGCAAGCAAGGATTTAGCATTCCTTGGGTGGGTGAACAAGT 1758
Db 1074 GGTAAAGSCAGATAGAAAGCAAGTGCAGAGCTTGCCTTCCCTGGGTCTCACAAGATGT 1133
Qy 1759 TGAGAGCTCATCAAAACAGAGAGGATCTCACTTTGTGAGTGTCTGCTCTCA 1812
Db 1134 TGAGAGGCTATTAAAGAGCAGAGGGAATCTTCTTTTGTGATGCTCAGCGCTCA 1187

RESULT 10

US-10-245-227B-13

; Sequence 13, Application US/10245227B

; Publication No. US20030200558A1

; GENERAL INFORMATION:

; APPLICANT: Rapp, William

; APPLICANT: Peng, Jixian

; APPLICANT: Nadiq, Gautham

; APPLICANT: Venkatesh, T

; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE

; FILE REFERENCE: REN-00-087-US
; CURRENT APPLICATION NUMBER: US/10/245,227B
; CURRENT FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: epitope form of beta-conglycinin beta-subunit
US-10-245-227B-13

Query Match 20.0%; Score 406.8; DB 7; Length 1278;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

Qy 562 GAACAACCCCTTTCTACTT---CCGTCAGGCGGTTTAGACCCGCTACGGGACCGCAAAA 618
Db 48 GAATAACCCCTTTCTACTTTGAGAAAGCTTAACAGCTTCCAAACTCTCTTTGAGAAACAAA 107
Qy 619 CGGTAGATCCGGGTCTCGCAGAGGTTTGACCAAGGTCAAGCGAGTTTCAGAAATCTCCA 678
Db 108 CGGTGCAATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACACTTGAGAACCTTCG 167
Qy 679 GAATCAACCGTATTTGTGCAGATCGAGGCCAAACCTTAACACTCTTTGTTCTTCCCAAGCACGC 738
Db 168 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCCCAACACAATCTTCTCCCCACCATGC 227
Qy 739 TGATGCTATAACATCTCTTGTATCCAGCAAGGGCAAGCCAGCTGACCGTAGCAATGG 798
Db 228 TGACGCGGATTTCTCTCTCTTTGTCTTAGCGGAGAGCCATACTTACCTTGGTGAACA 287
Qy 799 CAATAACAGAAAGAGCTTTAACTCTTCAGCGGSCATGCACCTCAGAAATCCCATCCGGTTT 858
Db 288 CGAGCAGAGACTCTTCAACCTTCACCTGGCGATGCCAGAGAAATCCAGCTGGAAC 347
Qy 859 CATTTCTCTACATCTTGAACCCGCTATGACAAACCAAGAACTTCAGAGTAGCTAAAAATCTCCAT 918
Db 348 CACTTACTATTTGTTTAACTTACCTCAGCACCCAGAAATCTCAAAATAATCAAACTTGCCAT 407
Qy 919 GCCGGTTAAACACACCCGCGCAGTTTGAAGATTTCTTCGCGGAGAGCAGCGGAGACCAATC 978
Db 408 ACCCGTCAACAAACCTTCGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 467
Qy 979 ATCTTACTTTCAGGGCTTCAGCAGGAATACGTTTGGAGGCGCCTTCAATCGCAATTCAA 1038
Db 468 GTCTTACTTTCAGGCTTCAGCCATTAATTTCTAGAGACCTCTCTTCCATAGCGAATTCGA 527
Qy 1039 TGAGATACGAGGAGGTCTGTTAGAAAGAAATGCAGGAGGTGAGCAAGAGAGAGAGGGCA 1098
Db 528 GGAGATAAACAGGTTTGTTCGGAGAGGAGAGAGAGCAGAGCAGCAAG----- 579
Qy 1099 GAGGCGATGGAGTACTTCGGAGTAGTGAGAAACAATGAAGAGTGATAGTCAAGGTGCAAA 1158
Db 580 -----GGAGTGATCGTGGAACTCTCAAA 602
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCACGCTAAATCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 603 GGAACAAATTCGGCAACTGAGCAGACGTGCAAAATCTAGTTCAAGGAAACCAATTTCTCTC 662
Qy 1219 AGAGGAGATATCACCAACCCCAATCACTTTGAGAGAGGCGAGCCCGATCTTTTCTAACAA 1278
Db 663 CGAAGATG-----AACCATTTCACTTGAGAACCCGCAACCCCATCTATTTCACAA 713
Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAAAGAAACCCCGAGCTTCAGAGCTTGA 1338
Db 714 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCCAACAGCTTCGGGACTTGA 770
Qy 1339 CATGATGCTCACCTGTGTAGATCAAGAGAGGCTTTGATGCTCCCACTTCAACTC 1398
Db 771 TATCTCTCTCAGTCTGTGGATATCAACGAAGAGGCTCTTCTTCTACCACTTCAATTC 830

Db 976 -----GAAGTGAAGGTACAGAGCTGAATTTGTCTGAAGACGATGTATT 1019
QY 1579 CATCATGCGAGCAGCTCATCCAGTAGCATCAACCGCTTCTCGAAGCTCCATCTGCTTGG 1638
Db 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACCGCTACCTCAAACTCTCAATTTCTTGC 1079
QY 1639 CTTGGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGAGGTGATAAGGACAATGT 1698
Db 1080 TTTTGGTATCAATGCTGAGAACCAACAGAGGAATCTCTTTCAGGCGAGAAAGACAATGT 1139
QY 1699 GATAGACAGATAGAGAGCAAGCAAGGATTTAGCAATTCCTGGGTGCGGTGAACAAT 1758
Db 1140 GGTAAAGCAGATAGAAAGCAAGTGCAGAGCTTGCCTTCCCTGGGTCTGCAAGATGT 1199
QY 1759 TGAGAGCTCATCAAAACAGAGGAAATCTCACTTTGTGAGTCTCGTCTCA 1812
Db 1200 TGAGAGCTATTAAAGAGCAGAGGGAATCTTACTTTGTGATGCTCAGCCTCA 1253

RESULT 12

US-10-245-227B-3

; Sequence 3, Application US/10245227B

; Publication No. US20030200558A1

; GENERAL INFORMATION:

; APPLICANT: Rapp, William

; APPLICANT: Peng, Jieixin

; APPLICANT: Nadiq, Gautham

; APPLICANT: Venkatesh, T

; TITLE OF INVENTION: ENHANCED PROTEINS AND METHODS FOR THEIR USE

; FILE REFERENCE: REN-00-087-US

; CURRENT APPLICATION NUMBER: US/10/245, 227B

; CURRENT FILING DATE: 2002-09-17

; NUMBER OF SEQ ID NOS: 83

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1320

; TYPE: DNA

; ORGANISM: Glycine max

US-10-245-227B-3

Query Match 20.08; Score 406.8; DB 7; Length 1320;

Best Local Similarity 62.14; Pred. No. 4.3e-115;

Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAACCCCTTCTACTT---CCGCTCAAGCGGTCTAGCACCGCTTACCGGGAACCAAAA 618
Db 90 GAATAACCCCTTCTACTTTGAGAAGCTCTAAGCTTCCAACTCTCTTTGAGAACCAAA 149
QY 619 CGGTAGATCCGGTCTGAGAGTTTGACAAAGTCAAGGAGTTTCAGAAATCTCCA 678
Db 150 CGGTGCGATTCGTCTCTCCAGAGATTCAACAAACGCTCCCAACACTTGAGAACCTTCG 209
QY 679 GAATACCGTATTGTGAGATCGAGCCCAACCTTAACACTTTGTTCTCCAGACGCG 738
Db 210 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCAACCAACTCTTCTCCCCACCATGC 269
QY 739 TGATGCTGATAACATCTCTGTTTCCAGCAAGGCAAGCCAGCTGACCGTAGCAATGG 798
Db 270 TGACGCGATTTCTCTCTCTTTGCTTACGGGAGGAGCCATCTACTTGTGTGAACA 329
QY 799 CAATAACAGAAAGAGCTTTTAATCTTGACGAGGCCATGCACTCAGAAATCCCGGTTT 858
Db 330 CGACGACAGAGACTCTCTACAACCTTCAACCTGCGATGCCAGAGAAATCCAGCTGGAAC 389
QY 859 CATTTCTACATCTTGACCGCATGACAAACCAAGCACTCAGAGTAGCTAAATCTCCAT 918
Db 390 CACTTACTATTGGTTTAACCTCTCAGCAACCAAGAAATCTCAAAATTAATCAAACTTCCAT 449
QY 919 GCCGTTTAAACACACCCCGGCTTTGAGGATTTCTTCCCGGCGAGAGCGGAGCAACAATC 978
Db 450 ACCGTCACAAACCTGGGAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 509
QY 979 ATCCTACTTGCAGGCTTACAGAGGAATACGTTGGAGGCGGCTTCAATGCGGAATTCAA 1038

Db 510 GTCTACTTGCAGAGGCTTCAAGCATAATATTCTAGAGACCTCTTCCATAGCAATTCGA 569
QY 1039 TGAGATACGAGGCTGCTGTTGAAGAGATGAGAGGTTGACAGAGAGAGAGAGGCA 1098
Db 570 GGAGATAAACACAGGTTTGTGGGAGGAGGAGGAGAGGAGGAGGAGGAGGAGGAGG 621
QY 1099 GAGCGATGAGTACTCGGAGTAGTGAGAACAAATGAAGGAGTAGTAGTCAAAAGTGTCAAA 1158
Db 622 -----GGAGTGTCTGGAACCTCTCAAA 644
QY 1159 GGAGCAGGTTGAAGAACTTACTAAGCAGCTTAATCGGTCTCAAGAAAGGCTCCGAAGA 1218
Db 645 GGAACAAATTCGCAACTGAGCAGAGCTGCAAAATCTAGTTCAAGGAGGAGGAGGAGGAGG 704
QY 1219 AGAGGAGATATCACCAACCAATCAATTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 1278
Db 705 CGAAGATG-----AACCATTTCACTTTGAGAGCGCAACCCATCTATTTCACAA 755
QY 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAAGAAAGAAACCCAGCTTCAGGACCTGGA 1338
Db 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAACCCACAGCTTCGGGACTTGGGA 812
QY 1339 CATGATGCTCACTGTGTAGAGATCAAGAGAGGAGCTTTGATGCTGCCACACTTCAACTC 1398
Db 813 TATCTTCTCAGTTCTGTGATATCAACGAAAGGAGCTCTTCTTCTACCACTTCAATTC 872
QY 1399 AAAGGCGATGTTATCGTCTGCTCAACAAAGAACTTGAAGAACTTGAACCTCTGGCTGT 1458
Db 873 AAAGGCGATGATGATCTAGTGATTAATGAAGGAGATGCAAACTTGAACCTTGTGGCAT 932
QY 1459 AAGAAAGAGCAACACAGAGGCGGCGGGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1518
Db 933 TAAAGAACCAACACAGACAGAAACAGGAAGAGAACTTTG----- 975
QY 1519 GGAGGAAAGTAACAGAGAGGTGCTAGGTACACAGCAGGTTGAAAGAGGCGCATGTGTT 1578
Db 976 -----GAAAGTCAAGAGGTACAGAGCTGAATTTGTCTCAAGACGATGTATT 1019
QY 1579 CATCATGCCAGAGCTCATCCAGTACCATCAACGCTTCTCCGAACTCCATCTGCTTGG 1638
Db 1020 TGTAAATTCAGCAGCTTATCCATTTGTCTCAACGCTACTCTAAACCTCAATTTCTTGC 1079
QY 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGGTTGATAAGGACAATGT 1698
Db 1080 TTTTGGTATCAATGCTGAGAACCAACAGAGGAACTTCTTTCAGGCGAGAGACAATGT 1139
QY 1699 GATAGACAGATAGAGAACCAAGCAGAGGATTTAGCATTTCCCTGGGTGCGGTGAACAATGT 1758
Db 1140 GGTAAAGCAGATAGAAAGACAAGTGCAGAGCTTGGCTTCCCTGGGTCTGCACAAGATGT 1199
QY 1759 TGAGAGGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTCTCGTCTCA 1812
Db 1200 TGAGAGGCTATTAAAGACAGAGGGAATCTTACTTTGTGATGCTCAGCCTCA 1253

RESULT 13

US-10-684-651-3

; Sequence 3, Application US/10684651

; Publication No. US20040064858A1

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; APPLICANT: GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-684-651-3

Query Match 20.0%; Score 406.8; DB 8; Length 1320;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAACCTTCTACTT---CCGTCAGGCGGTTTAGCACCGCTACGGGAAACCAAAA 618
DB 90 GAATAACCTTCTACTTTAGAGCTCTAACAGCTTCCAACTCTCTTTGAGAACCAAAA 149
QY 619 CGGTAGATCCGGGTCTCTGAGAGGTTTGACAAAGGTCAAGGAGTTTCAGAAATCTCCA 678
DB 150 CGTTGCGATTCGTCTCTCCAGAGATTCAACAAAGCTCCCAACAACTTGAGAACTTCG 209
QY 679 GAATACCGTATTTGTCAGATCAGGCAAACTTAACACTCTTGTCTTCCCAAGCAGC 738
DB 210 AGACTACCGGATTTGTCAGTTTCAGTCAAAACCCAAACACAACTCTCTCCCAACCATGC 269
QY 739 TGATGCTGATAACATCTCTGTTATCCAGCAAGGGCAAGCCACCGTGACCGTAGCAAAATGG 798
DB 270 TGACGCGATTCTCTCTCTTTGCTCTTAGCGGAGAGCCATACCTTGTGTGAACAA 329
QY 799 CAATAACAGAAAGAGCTTTAATCTTGACGAGGCCATGCACTCAGAAATCCCATCCGGTTT 858
DB 330 CGACGACAGAGACTCTTACAACCTTCAACCTGCGATGCCAGAGAAATCCAGCTGGAAC 389
QY 859 CATTTCTACATCTTGAACCGCCATGACACACGAGACCTCAGAGTAGCTAAATCTCCAT 918
DB 390 CACTTACTATTGTTGTTAACTTCAACACCAACCAAGAACTCTCAAAATTAATCAAACTTCCCAT 449
QY 919 GCCCGTTAACACACCGCGGCTTTCAGGATTTCTCCCGGCGAGCGGAGACCAATC 978
DB 450 ACCCGTCAACAACTTGGGAGATATGATGATTTCTTCTATCTAGCACTCAAGCCCAACA 509
QY 979 ATCTTACTTGCAGGGTTTACGAGGAATACGTTGGAGGCGCTTCAATGCGGAATTCAA 1038
DB 510 GTCTTACTTGAAGGTTTACGCCATAATATTTAGAGACCTCTCCATAGCGAAATTCGA 569
QY 1039 TGAGATACGAGGTTGCTGTTAGACGAGATGAGGAGGTGACAGAGGAGAGAGGCA 1098
DB 570 GGAGATAAACAGGGTTTGTGTTGGAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGG 621
QY 1099 GAGGCGATGAGTAGTCTCGGAGTAGTGAGAAACAATGAAGGAGTAGTAGTCAAAAGTGTCAA 1158

DB 622 -----GGAGTGATCGTGAACCTCTCAAA 644
QY 1159 GGAGCACGTTGAGAACTTTACTAAGCACGCTAAATCCGTCTCAAGAAAGGCTCCGAAGA 1218
DB 645 GGAACAAATTCGCAACTGAGCAGAGCTGCCAAATCTAGTTCAAGGAAACCAATTTCTCTC 704
QY 1219 AGAGGAGATATCACCAACCCCAATCAACTTGAGAGAGGCGGAGCCGATCTTTCTTAACAA 1278
DB 705 CGAAGATG-----AACCAATTCAACTTGAGAGCCGCAACCCCATCTTATTTCCAACAA 755
QY 1279 CTTTGGGAAAGTTATTTGAGGTGAAGCGACAGCAAGAAAGAAACCCCGAGCTTTCAGGACCTGGA 1338
DB 756 CTTTGGAAAGTTCTTTGAGATCACCCCTG---AGAAAAACCCACAGCTTCGGGACTTGA 812
QY 1339 CATGATGCTCACTGTGTAGAGATCAAGAGAGAGCTTTGATGCTCCCACTTCAAACTC 1398
DB 813 TATCTTCTCTCAGTTCTGTGGATATCAACGAAAGAGCTCTTCTTACCACACTTCAATTC 872
QY 1399 AAAGGCCATGGTTATCGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1458
DB 873 AAAGGCCATAGTGATACTAGTGATTAATGAAGGAGATGCAAAACATTTGAACCTTGTTCG 932
QY 1459 AAGAAAGAGCAACAAACAGAGGGGCGCGGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 1518
DB 933 TAAAGNACAACAACAGAGAGCAAGAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
QY 1519 GGAGGGAAGTAACAGAGAGGTCGTAGGTACACAGGAGGTTGAGAGGAGGAGGAGGAGGAG 1578
DB 976 -----GAAAGTCAAAAGGTACAGAGCTGAATTTCTCTGAAAGAGGATGATTT 1019
QY 1579 CATATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTGCTCG 1638
DB 1020 TGTAATTCAGCAGCTTATTCATTTGTCGTCACGCTACTCTCAAACTCAATTTCTCTGCT 1079
QY 1639 CTTTGGTATCAACCGCTGAAACAAACCAAGAAATCTTCTTTCGAGGTGATAAGGACAATGT 1698
DB 1080 TTTTGGTATCAATGCTGAGACAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139
QY 1699 GATAGACAGATAGAGAGCAAGCAGAGGATTTAGCATTCCTTGGGTCGGGTGGAACAAGT 1758
DB 1140 GGTAAAGCAGATAGAAAGCAAGTGCAGAGCTTGCCTTCCCTGGGTCTGCAACAAGATGT 1199
QY 1759 TGAGAGCTCATCAAAACCAAGAGAACTCTCACTTTGTGAGTGTCTGCTCTCA 1812
DB 1200 TGAGAGCTTATTAAGAGCAGAGGAACTCTTCTTGTGATGCTCAGCCTCA 1253

RESULT 14

US-10-757-074-3
; Sequence 3, Application US/10757074
; Publication No. US20040139502A1
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/757,074

; FILING DATE: 14-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1320 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-757-074-3

Query Match 20.0%; Score 406.8; DB 8; Length 1320;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

QY 562 GAACAAACCTTTCTACTT---CCGTCAGGCGTTTAGCACCGCTACCGGACCAAAA 618
DB 90 GAATAACCTTTCTACTTTAGAGCTCTAACAGCTTCCAAACTCTCTTTGAGAACCAAAA 149
QY 619 CGGTAGGATCCGGTCTCGCAGAGGTTTGACCAAGGTCAAGGCAGTTTCAGAAATCTCCA 678
DB 150 CGTTCGATTCGTCCTCTCAGAGATTCAACAAACGCTCCCCACAACTTGAGAACCTTCG 209
QY 679 GAATACCGTATTGTGCAGATCGAGGCCAAACCTTAACACTCTTTGTTTCCCAAGCAGC 738
DB 210 AGACTACCGGATTGTCAGTTTCAGTCAAAACCAACACAAATCTCTCCCCCAACCATGC 269
QY 739 TGATGCTGATAACATCTCTGTTATCCAGCAAGGCCAGCCAGCTGACCGTAGCAATGG 798
DB 270 TGACGCGGATTTCTCTCTTTGTCCTTAGCGGAGAGCCATCTTACCTTTGTTGACAA 329
QY 799 CAATAACAGAAAGAGCTTTAATCTTGACAGGGCCATGCACTCAGAAATCCCATCCGTTT 858
DB 330 CGAGCAGAGAGCTCTTACAACTTTCACCTGGCGATGCCAGAGAAATCCAGCTGGAAC 389
QY 859 CATTTCTCATCTTGTAACCGCCATGACAAACCAAGCTCAGAGTAGCTAAATCTCCAT 918
DB 390 CACTTACTATTGGTTAACTTACCTCAGACACCAGAAATCTCAAAATATCAAACTTGCCAT 449
QY 919 GCCGTTAAACACACCGCCGAGTTTGGAGATTCTTCCCGGAGAGCCAGACCAATC 978
DB 450 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTATCTAGCACTCAAGCCCAACA 509
QY 979 ATCTTCTTCAGGCTTTCAGCAGGAATACGTTGGAGCGCGCTTCAATCGGAATTCAA 1038
DB 510 GTCTTCTTGAAGGCTTCAGCCATAATATCTAGAGACTCTCTTCCATAGCAATTCGA 569
QY 1039 TGAGATACGAGGGTGTGTTAGAGAGAAATGCAAGGAGGTGAGCAGAGGAGAGGGCA 1098
DB 570 GGAGATAACAGGGTTTGTGAGAGGAAGAGGAGCAGGAGCAGCAAG----- 621
QY 1099 GAGCGGATGGAGTACTCGGAGTAGTGAGAAATGAAGGAGTAGTAGTCAAGTGTCAAA 1158
DB 622 -----GGAGTGTCTGTGGAATCTCAAA 644
QY 1159 GGAGCAGCTTGAGAACTTACTAGCAGCTTAATCGTCTCAAGAAAGGCTCCGAAGA 1218
DB 645 GGAACAAATTCGGCAATCTAGCAGAGCTGCAAACTTAGTTCAAGGAAACCAATTTCTC 704
QY 1219 AGAGGAGATATCACCACCAATCAACTTTGAGAGAGGCGAGCCCGATCTTTCTAACA 1278

DB 705 CGAAGATG-----AACCATTTCAACTTGAGAACCGCAACCCCATCTTATTTCCACAA 755
QY 1279 CTTTGGGAAGTTATTTGAGTGAAGCAGACAAGAAAGAACCCCGAGCTTCAGGACCTGGA 1338
DB 756 CTTTGGAAAGTTCTTTGAGATCACCCTG---AGAAAACCCACAGCTTCGGGACTTGA 812
QY 1339 CATGATGCTCACCTGTGTAGAGATCAAGAGAGGCTTTTGTATGCTCCACACTTCAACTC 1398
DB 813 TATCTTCTCAGTTCTGTGATATCAACGAAGGAGCTCTTCTTCTACCACTTCAATTC 872
QY 1399 AAAGGCATGGTTATCGTGTCTCAACAAAGAACTGGAACCTTGAACCTCGTGTGT 1458
DB 873 AAAGGCATAGTGATATACTAGTGATTAAAGAGAGATGCAAAACATTTGAACCTTGTGGCAT 932
QY 1459 AAGAAAAGAGCAACAACAGAGGGGCGCGGGAAGAGAGGAGGAGCAAGACGAAGAAGA 1518
DB 933 TAAAGAACACACAACAGAGCAAGAAACAGGAGAGGAACTTTG----- 975
QY 1519 GGAGGGAAGTAAACAGAGAGGTGCGTAGGTACACAGCGAGGTTGAAGGAAGCGGATGTT 1578
DB 976 -----GAAGTGCAAGGTACAGAGCTGAATTTGCTGAAGACGATGATT 1019
QY 1579 CATCATGCCAGAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACCTCCATCTGCTGG 1638
DB 1020 TGTAAATTCAGCAGCTTATCCATTTGTCGTCAACGCTACCTCAAACTTCAATTTCTTGC 1079
QY 1639 CTTTCGGTATCAACGCTGAAACCAACACAGAAATCTTCTTTCAGAGGTGATAAGGACAATGT 1698
DB 1080 TTTTGTATCAATGCTGAGAACCAACAGAGGAACTTCTTTCAGGCGGAGAAACAATGT 1139
QY 1699 GATAGACCAAGATAGAGAAGCAAGCAAGAGGATTTAGCATTTCCCTGGGTGGAACAAGT 1758
DB 1140 GGTAAAGCAGATAGAAAGACAAGTGCAGGAGCTTGCCTTCCCTGGGTCTGCACAAGATGT 1199
QY 1759 TGAGAAGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812
DB 1200 TGAGAGGCTATTAAAGAGCAGAGGGAATCTACTTTGTGTGATGCTCAGCCTCA 1253

RESULT 15

US-10-757-155-3

; Sequence 3, Application US/10757155

; Publication No. US20040139503A1

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/757,155

; FILING DATE: 14-Jan-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/758,652

; FILING DATE: 11-Jan-2001

; APPLICATION NUMBER: 60/019,940

; FILING DATE: JUNE 14, 1996

; ATTORNEY/AGENT INFORMATION:

```
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1320 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-757-155-3

Query Match      20.0%; Score 406.8; DB 8; Length 1320;
Best Local Similarity 62.1%; Pred. No. 4.3e-115;
Matches 779; Conservative 0; Mismatches 382; Indels 93; Gaps 5;

Qy 562 GAACAACCCCTTCTACTT-----CCCGTCAAGCGGTTTAGACCCGCTACGGGAAACCAAA 618
Db 90 GAATAACCCCTTCTACTTTAGAGCTCTAACAGCTTCAAACTCTCTTTGAGAAACCAAA 149
Qy 619 CGGTAGGATCCGGTCTCTGAGAGGTTTGACCAAGGTCAAGGAGTTTCAGBAATCTCCA 678
Db 150 CGTTCGCAATTCGCTCTCTCAGAGATTCAACAACCGCTCCCACTTTGAGAAACCTTCG 209
Qy 679 GAATACCCGTTATTTGTCAGATCGAGGCCAAACCTTAACACTCTTTGTTCTTCCCAAGCACGC 738
Db 210 AGACTACCGGATTGTCAGTTTCAGTCAAAACCAACCAACATCTTCTCCCAACCATGC 269
Qy 739 TGATGCTGATAACATCTCTGTTATTCAGCAAGGCAAGGCAAGCCGTCAGCTAGCAATGG 798
Db 270 TGACGCGGATTTCTCTCTCTTCTGCTTTAGCGGAGAGCCATCTTACCTTTGTTGAACAA 329
Qy 799 CAATAACAGAAAGAGCTTTTAATCTTGACGAGGCCATGCACTCAGAAATCCCATCCCGTTT 858
Db 330 CGACGACAGAGATCTCTTACAACTTTCACCTGCGGATGCCAGAGAAATCCAGCTGGAAC 389
Qy 859 CATTCCTTACATCTTGAACCGCCATGACAAACAGAACTCAGAGTAGCTAAATCTCCAT 918
Db 390 CACTTACTATTGTTTAACTTCAAGCCACACAGAACTCAAAATTAATCAAACTTCCAT 449
Qy 919 GCCCGTTAACAACCCGCGCAGTTTGAGGATTTCTCCGCGGAGGAGCGGAGACCAATC 978
Db 450 ACCCGTCAACAAACCTGGCAGATATGATGATTTCTTCTTATCTAGCACTCAAGCCCAACA 509
Qy 979 ATCTTACTTGCAGGCTTTCAGCAGGAATACGTTGGAGGCGCCTTCAATGCGGAATTCAA 1038
Db 510 GTCTTACTTGAAGGCTTTCAGCCATTAATTTCTAGAGACCTCTTCCATAGCGAATTCGA 569
Qy 1039 TGAGATACGAGGAGGTGCTGTTAGAGAGAAATGACAGAGGTGAGCAAGAGAGAGAGGCA 1098
Db 570 GGAGATAAACAGGGTTTTGTTTGAGAGGAAGAGGAGCAGAGCAGCAAGAG----- 621
Qy 1099 GAGCGATGGAGTACTCGGAGTAGTGAGAAATGAGAGGTGATAGTCAAGTGTCAA 1158
Db 622 -----GGAGTGTCTGTGGAACTCTCAAA 644
Qy 1159 GGAGCAGGTTGAAGAACTTACTAAGCACGCTAAATCCGTCTCAAGAAAGGCTCCGAAGA 1218
Db 645 GGAAACAAATTCGGCAACTGAGCAGAGCTGCCAAATCTAGTTCAAGGAAACCAATTCCTC 704
Qy 1219 AGAGGAGAGATATCAACCAACCAATCAACTTGAGAGAGGCGAGCCCGATCTTTCTAACAA 1278
Db 705 CGAAGATG-----AACCAATTCACTTGAGAGCGGCAACCCCATCTATTCCAACAA 755
Qy 1279 CTTTGGGAAGTTATTTGAGGTGAAGCCAGACAGAGAAACCCCGAGTTTCAGGACCTGGA 1338
Db 756 CTTTGGAAAGTTCTTTGAGATCACCCTG---AGAAACCCACAGCTTCGGGACTTGGGA 812
Qy 1339 CATGATGCTCACCTGTGTAGAGATCAAGAAAGGAGCTTTTGATGCTCCCACTTCAACTC 1398
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Db 813 TATCTTCTCAGTTCTGTGATATCAACGAAGAGCTCTTCTTACCACTTCAATTC 872
Qy 1399 AAAGGCCATGGTTATCGTCTCGTCAACAAAGGAACTGGAACCTTTGAACTCGTGCTGT 1458
Db 873 AAAGGCCATAGTCATATACTAGTATTAAATGAAGAGATGCAAAACATTGAACTTGTTCGCAT 932
Qy 1459 AAGAAAGAGCAACAAACAGAGGGGACGGCGGGAAGAAAGAGGAGGACGAAGACGAAGAAGA 1518
Db 933 TAAAGAAACAAACAAACAGAGCAGAAAAACAGGAAGAGGAAACCTTTG----- 975
Qy 1519 GGAGGAAAGTAACAGAGAGGTCGTAGGTACACAGAGGAGTTGAAGGAAGGCGATGTT 1578
Db 976 -----GAAAGTGCAAAGGTACAGAGCTGAATTTGTCTGAAAGACGATGATT 1019
Qy 1579 CATCATGCCAGCAGCTCATCCAGTAGCCATCAACGCTTCTCCGAACTCCATCTGCTTG 1638
Db 1020 TGTAAATTCAGCAGCTTATCCATTTTGTCTCAACGCTACCTCAAACTCAATTTCTTGC 1079
Qy 1639 CTTTCGTTATCAACGCTGAAACAAACCAACAGAAATCTTCTTGCAGGTGATAAGGACAATGT 1698
Db 1080 TTTTGGTATCAATGTCTGAGAACAAACCAAGAGAACTTCTTTCGAGGCGAGAAACAAATGT 1139
Qy 1699 GATAGACCAGATAGAGAAGCAAGCGAAGGATTTAGCATTTCCCTGGGTCCGGTGAAACAAGT 1758
Db 1140 GGTAAAGCAGATAGAAAGACAAAGTGCAGGAGCTTGGCTTCCCTGGGTCTGCACAGATGT 1199
Qy 1759 TGAGAAGCTCATCAAAACCAAGAGGAATCTCACTTTGTGAGTGTCTGCTCTCA 1812
Db 1200 TGAGAGGCTATTAAAGAGCAGAGGGAATCTCTACTTTGTTGATGCTCAGCCTCA 1253
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Search completed: June 24, 2006, 01:56:13

Job time : 2781.65 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:21:18 ; Search time 44.2256 Seconds
(without alignments)
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Perfect score: 2032
Sequence: 1 aataatcatatattatc.....cgtttggtggtttcttc 2032

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /EMC_Celerra_SID33/prodata/1/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SID33/prodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SID33/prodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SID33/prodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SID33/prodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SID33/prodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SID33/prodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SID33/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58.6	2.9	1338	6	US-10-953-349-26870
2	46.6	2.3	1005	6	US-10-449-902-25812
3	43.4	2.1	1295	6	US-10-449-902-20667
4	42.2	2.1	1420	6	US-10-534-744-1
5	42	2.1	726	6	US-10-953-349-34378
6	41.6	2.0	931	6	US-10-449-902-6550
7	41.4	2.0	1644	6	US-10-953-349-38190
8	40.8	2.0	3602	6	US-10-449-902-9830
9	40.4	2.0	615	7	US-11-217-529-77435
10	40.4	2.0	3489	7	US-11-106-014-93
11	39.2	1.9	1962	6	US-10-486-020-52
12	39.2	1.9	2824	6	US-10-486-020-48
13	39.2	1.9	2906	6	US-10-486-020-54
14	39.2	1.9	3005	6	US-10-486-020-53
15	39.2	1.9	3495	7	US-11-217-529-5994
16	39	1.9	2140	6	US-10-449-902-25837
17	38.8	1.9	653	6	US-10-449-902-5672
18	38.6	1.9	42999	7	US-11-284-877-17
19	38	1.9	151830	6	US-10-519-335-37
20	37.6	1.9	1539	6	US-10-953-349-23883
21	37.6	1.9	2824	7	US-11-293-697-93
22	37.4	1.8	735	6	US-10-449-902-10416
23	37.2	1.8	1045	6	US-10-953-349-26209
24	37	1.8	547	6	US-10-488-619-2599
25	37	1.8	776	6	US-10-488-619-1733

ALIGNMENTS

RESULT 1

US-10-953-349-26870
; Sequence 26870, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26870
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-10-953-349-26870

Query Match 2.9%; Score 58.6; DB 6; Length 1338;
Best Local Similarity 47.0%; Pred. No. 2.2e+07;
Matches 181; Conservative 0; Mismatches 204; Indels 0; Gaps 0;

QY	569	CCTTTCTACTTCCCGTCAAGGGGTTTAGCACCCGCTACGGGAACCAAAACGGTAGATC	628	Sequence 13170, A
DB	436	CGGTACGTTTCGGCCCGCGCAGCTTCCCGCGCATCATCGGAGCGACACGGGTTTCGTC	495	Sequence 25812, A
QY	629	CGGTCTCTCAGAGTTTTCACCAAGGTCAGGCAATTCAGAAATCTCCAGATCACCGT	688	Sequence 18644, A
DB	496	AAGGCCCTTCGCGCGTTCGACGAAGTGTCCAGGCTCCTCCGGGGCATCAGAAATACCGT	555	Sequence 9874, Ap
QY	689	ATTGTGCAGATCGAGCCAAACCTAACACTTGTTCCTCCCAAGCACGCTGATGCTGAT	748	Sequence 8264, Ap
DB	556	GTCCGCATCATGAGGTGAACCCGCGCGGTTCGTCGTCGGGATCTACGGAGGAGAC	615	Sequence 22022, A
QY	749	AACATCTTTTATCCAGCAAGGCAAGCCCGTAGCCGTAACAAATGSCAAATAACAGA	808	Sequence 23827, A
DB	616	GGCGTCGGTACGTCGCTCAAGCGAGGGGTGCTGACGGTGTGATCGAAGACGGCGAGAAG	675	Sequence 17345, A
QY	809	AGAGCTTTTAATCTTACGAGGGCCATGGCACTCAGAAATCCATCCCGTTTCATTCCTAC	868	Sequence 19173, A
DB	676	CGGTCTCTACACCGCTCAGGAAGCGATGTGATCGTGGCCCGCGGGTCCATCATGCAC	735	Sequence 5628, Ap
QY	869	ATCTTCAACCGGCATGACAACAGAACCTCAGAGTAGTAAAAATCTCCATGCCCGTTAAC	928	Sequence 17797, A
DB	736	CTGGCCAAACACGACCGCGGAGGAAGCTGTGATCATGCCAAGATTTCCACACCATCTCC	795	Sequence 1913, Ap
QY	929	ACACCGCGCAGTTTGAGGATTCT 953		Sequence 20711, A

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Db 796 GTCCCGGCAAGTTCAGTATTCT 820

RESULT 2
US-10-449-902-7999
; Sequence 7999, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7999
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105347
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-7999

Query Match 2.3%; Score 46.6; DB 6; Length 1005;
Best Local Similarity 46.0%; Pred. No. 0.00068;
Matches 157; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 607 CGGGRACCAACGCTAGGATCGGCTCTGACAGAGTTTGACCAAGGTCAAGGAGTT 666
Db 396 CGCAGGACCAAGGCTCGCTAGGCTCTCCCGCGCTTCCACAGGCGTCCAGCTCCT 455
QY 667 TCAGAAATCTCCAGAAATCACCGTATTGTGCAGATCGAGGCGCAACCTTAAACACTCTTGTCT 726
Db 456 GC CGCGGATCAAGAACTACCGCTCGCGGTGCTCGAGGGAACCCGCGCTCTTCTCAT 515
QY 727 TCCAGACGCTGATGCTGATTAACATCTTGTATTATCCAGCAAGGCGGACCGGTGAC 786
Db 516 GCGGACCCACACGACGCGCACTGCTCTGCTACGTCGCGCAAGGCGGAGGTGTTGGC 575
QY 787 CGTAGCAATGCGCAATAACAGAAAGAGCTTTAATCTTGACGAGGCGCATGCACTCAGAA 846
Db 576 GATCATCGAAGCGCGGAGAAAGTGTGTCGTACGCCATCCGCAAGGCGACGTCTTCTGGC 635
QY 847 CCATCCGGTTTCATTCTTACATCTTTGAAACCGCCATGACCAACAGAACTTCAGATGAC 906
Db 636 GCGCGGGGACGATCAATTTACTTGGCAACACCGAGCGCGGAGGAAGTGTATCTGTTAC 695
QY 907 TAAATCTCATCGCGCTTAAACACACCCGCGCGAGTTTGGG 947
Db 696 CAAGATTCTCATACCATCTCCGTCCTCGTGGCCAGATCCAGG 736

RESULT 3
US-10-449-902-20667
; Sequence 20667, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7999
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105347
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-7999

; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20667
; LENGTH: 1295
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070973
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-20667

Query Match 2.1%; Score 43.4; DB 6; Length 1295;
Best Local Similarity 53.9%; Pred. No. 0.0071;
Matches 89; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 373 AAGAGAGGAGGAGCGCGATGGGGACCACTGGACCGAGGGAGCGTGAAGAGAGAAAGA 432
Db 543 AAGAAAGAGAAAGACACAGAGTGTATAGAGGAGAGAGGCAAGAAAAAGGATGGTG 602
QY 433 CTGGAGACACCAAGAGAGAGATTGGAGGCGCAACAGTCTCAGCAGCCCGGAAAAATAAG 492
Db 603 ATGAGGAGGAAGGTAAAGAAAGAAAGAAAGAAAGAAAGATGCGGATGAGAAAGAG 662
QY 493 GCCCGAAGGAGAGAGGAGGAGAAACAAGAGTGGGGGAAACACCAGGTTAG 537
Db 663 GCAAGAAAGAGAGAGGAGGAGGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 707

RESULT 4
US-10-534-744-1
; Sequence 1, Application US/10534744
; Publication No. US2006012375A1
; GENERAL INFORMATION:
; APPLICANT: University of Saskatchewan Technologies Inc.
; TITLE OF INVENTION: PLANT STRESS TOLERANCE GENES, AND USES THEREFOR
; FILE REFERENCE: 47968-PT
; CURRENT APPLICATION NUMBER: US/10/534,744
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 60/426,012
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1420
; TYPE: DNA
; ORGANISM: Bromus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1212)..(1212)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (77)..(1231)
; OTHER INFORMATION:
; US-10-534-744-1

Query Match 2.1%; Score 42.2; DB 6; Length 1420;
Best Local Similarity 50.5%; Pred. No. 0.017;
Matches 101; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 329 GGCGCCCAACCCGGAGACTACGATGATGACCCCGCTCAACCCCGAAGAGAGAGGAGGC 388
Db 1030 GGACGCCACGTTGGAGAGACCGAGTCCGCGAAGGAGCGCGCTTGGAGACGCGGAGGC 1089
QY 389 CGATGGGGACCACTGGACCGAGGGAGCGTGAAGAGAGAGAGACTGGAGACACCAAGA 448
Db 1090 GGCCAAAGGGCAAGGCTTAACGAGGGGTACGAGAAGGTGAAGGAGAGGAGCGGACCAAGGA 1149
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Db 436 GCGCCGTCGTGTAAGTCTCGGCACACGACCAAGTCGGAAGTGTCCGGCTGCTATGCTCC 495
QY 915 CCATGCC---CGTTAAACACACCCGCGCAGTTTGGAGATTCTTCCCGGCGAGCAGCCGAG 971
Db 496 TCAGCCCGCGTCGCTCCAGCTCTGGACGCTTCGAGGAGTCTTCCCCCATCGGAGGCGAGA 555
QY 972 ACCAATCATCTACTTTCAGCGGCTTCAGCAAGGAATAGTTGGAGCGCGCTTCAA 1026
Db 556 GCGCCGAGTCTTCTCTCAGCGTCTTCAGCGACGACGCTTATCCAGGCGGTCTGTTCAA 610

RESULT 8

US-10-449-902-9830
; Sequence 9830, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9830
; LENGTH: 3602
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107178
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9830

Query Match 2.0%; Score 40.8; DB 6; Length 3602;
Best Local Similarity 48.3%; Pred. No. 0.081;
Matches 114; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 269 GATCTCTGAGGACACACTGCGACACCAACCAAGTTCCTCCAGGGAGCGGACAGT 328
Db 280 GAGGCTGGCGCCCAAGCGCGGAAGCGCTCCATCTGTCGAGCTCTTCGCGCGCTGCCAA 339
QY 329 GCGCGCAACCCGCGAGACTACGATGATGACCGCGTCAACCCGAGAGAGGAGGCG 388
Db 340 GGTCTGTCGCGCCCGCGACGAGGGCTCGGAGGGGAGCGGTGTGAGGAGGAGCTCGA 399
QY 389 CGATGGGACACCTGCGACGCGAGCGTGAAGAGAGAGAGACTGGAGACACCAAGA 448
Db 400 CAAGGGGACCCCGCGCGTGGGTGAGGCGGCGAAGAGAGGGTTCAGGAAGCA 459
QY 449 GAAGATTGAGGCGACCAAGTCTATCAGCACCGCAAGAAATAAGGCCCGCAAGAG 504
Db 460 GAAGTTTCTAGTTGAGATCGGCTCAGAAAAAAGGAGAAAAATAGCAAGACAAAG 515

RESULT 9

US-11-217-529-77435/c
; Sequence 77435, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77435
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (152)..(192)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-77435

Query Match 2.0%; Score 40.4; DB 7; Length 615;
Best Local Similarity 53.1%; Pred. No. 0.035;
Matches 86; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 373 AAGAGAGGAGGAGCGCGATGGGACCGAGCTGGACCGAGGCGTGAAGAGAGAA 432
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QY 433 CTGGACACACCAAGAGAGAGATTGGAGGCGGACCAAGTCTCAGCAGCCCGGAAATAAG 492
Db 294 AAGATGAAGAAATAAAGAAAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAG 235
QY 493 GCGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 534
Db 234 AAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 193

RESULT 10

US-11-106-014-93
; Sequence 93, Application US/11106014
; Publication No. US2006008846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiau, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Srivastava, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Fbx1 11 protein (NP_036440.1)
US-11-106-014-93

Query Match 2.0%; Score 40.4; DB 7; Length 3489;
Best Local Similarity 65.6%; Pred. No. 0.1;

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: June 23, 2006, 09:32:31 ; Search time 4184.37 Seconds
(without alignments)
10957.506 Million cell updates/sec
Title: US-10-728-051-2
Perfect score: 717
Sequence: 1 gctcaccatactagtagcccc.....taaaaagatcatgttttggtt 717
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_pat.*
3: gb_ph.*
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5: gb_pr.*
6: gb_ro.*
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8: gb_sy.*
9: gb_un.*
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13: gb_in.*
14: gb_om.*
15: gb_ba.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
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2	717	100.0	717 2 AR629099 Sequence
3	717	100.0	717 2 AR629100 Sequence
4	717	100.0	717 4 ARQALL11
5	713.8	99.6	743 2 AR257462 Sequence
6	705	98.3	810 4 AY722689
7	644.6	89.9	842 4 AY581853
8	598.8	83.5	678 4 AY581854
9	474	66.1	474 2 BD107899
10	472.4	65.9	474 2 AX155333
11	470.8	65.7	474 2 BD172108
12	462	64.4	472 4 AY007229
13	462	64.4	682 2 AR716327
14	462	64.4	682 2 AX148740
15	462	64.4	1162 2 AR716326
16	462	64.4	1162 2 AX148738
17	419.4	58.5	519 4 AY158467
18	415.2	57.9	510 4 AY117434

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21	220.8	30.8	634	4	AF366561	Arachis h
22	202.2	28.2	742	4	AY722690	Arachis h
23	197.8	27.6	627	4	AF092846	Arachis h
24	181.6	25.3	618	4	AY848699	Arachis h
25	162.6	22.7	375	4	AY871100	Arachis h
26	114.8	16.0	712	4	AF091737	Arachis h
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ALIGNMENTS

RESULT 1
AR257468
LOCUS AR257468 717 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 20 from patent US 6486311.
ACCESSION AR257468
VERSION AR257468.1 GI:27307481
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 717)
AUTHORS Burks,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A., Helm,R.M. and Bannon,G.A.
TITLE Peanut allergens and methods
JOURNAL Patent: US 6486311-A 20 26-NOV-2002;
NY Mc. Sinai School of Medicine and University of Arkansas; New York.
FEATURES
source NY Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 717; DB 2; Length 717;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCACCATACTAGTAGCCCTGCCCTTTTCTCTCGCTGCCACGCATCTCGGAGGCA 60
DB 1 GCTCACCATACTAGTAGCCCTGCCCTTTTCTCTCGCTGCCACGCATCTCGGAGGCA 60
QY 61 GCAGTGGGAACCTCCAAGGACAGAGATGCCAGAGCCAGCTCGAGAGCGCAACCTGAG 120
DB 61 GCAGTGGGAACCTCCAAGGACAGAGATGCCAGAGCCAGCTCGAGAGCGCAACCTGAG 120
QY 121 GCCCTCGGAGCAACATCTTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA 180
DB 121 GCCCTCGGAGCAACATCTTCATGCAGAAGATCCAACGTGACGAGGATTCATATGAACGGGA 180
QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 240

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Db 181 CCGGTACAGCCCTAGTCAGAGTCCGTTACAGCCCTAGTCCATATGATCGGAGGCGCGTGG 240
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RESULT 2
AR629099 LOCUS 717 bp mRNA linear PAT 14-FEB-2005
DEFINITION Sequence 6 from patent US 6835824.
ACCESSION AR629099
VERSION AR629099.1 GI:59756575
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 717)
AUTHORS Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.
TITLE Peanut allergens and methods
JOURNAL Patent: US 6835824-A 6 28-DEC-2004;
Location/Qualifiers Little Rock, AR
FEATURES
source 1. .717
/mol_type="mRNA"
ORIGIN
Query Match 100.0%; Score 717; DB 2; Length 717;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCAGCGCATCTGGAGGCA 60
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCGCTGCCAGCGCATCTGGAGGCA 60
Qy 61 GCAGTGGGAATCCCAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
Db 61 GCAGTGGGAATCCCAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
Qy 121 GCCTCGCAGCAACATCTCATATGCAAGAGATCCAAACGTTGACGAGATTCATATGAACGGGA 180
Db 121 GCCTCGCAGCAACATCTCATATGCAAGAGATCCAAACGTTGACGAGATTCATATGAACGGGA 180
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Qy 181 CCGGTACAGCCCTAGTCAGAGTCCGTTACAGCCCTAGTCCATATGATCGGAGGCGCGTGG 240
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RESULT 3
AR629100 LOCUS 717 bp mRNA linear PAT 14-FEB-2005
DEFINITION Sequence 9 from patent US 6835824.
ACCESSION AR629100
VERSION AR629100.1 GI:59756577
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 717)
AUTHORS Burks,A.W. Jr., Stanley,J.S., Bannon,G.A., Cockrell,G. and Helm,R.M.
TITLE Peanut allergens and methods
JOURNAL Patent: US 6835824-A 9 28-DEC-2004;
Location/Qualifiers Little Rock, AR
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source 1. .717
/mol_type="mRNA"
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Query Match 100.0%; Score 717; DB 2; Length 717;
Best Local Similarity 100.0%; Pred. No. 9e-202;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 GCCTCGCAGCAACATCTCATATGCAAGAGATCCAAACGTTGACGAGATTCATATGAACGGGA 180
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Db 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTTGTT 717

RESULT 4
ARQALLII
LOCUS Arachis hypogaea (clone Ara h II p38) allergen II gene, polyA
DEFINITION signal.

ACCESSION L77197.1 GI:1236995
VERSION 1
KEYWORDS allergen; conglutin; seed storage protein.
SOURCE Arachis hypogaea (peanut)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 717)

AUTHORS Stanley,J.S.

TITLE The major peanut allergen Ara h II is a seed storage protein with

multiple IgE-binding epitopes

JOURNAL Unpublished (1996)

COMMENT Original source text: Arachis hypogaea (strain Florunner) (clone: Ara h II p38) DNA.

FEATURES

source

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/organism="Arachis hypogaea"

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ORIGIN

Query Match 100.0%; Score 717; DB 4; Length 717;

Best Local Similarity 100.0%; Pred. No. 9e-202;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5

AR257462

LOCUS

DEFINITION

Sequence 1 from patent US 6486311.

AR257462

ACCESSION

VERSION

AR257462.1 GI:27307475

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 743)

AUTHORS

Burke,A.W. Jr., Stanley,J.S., Cockrell,G., King,N.E., Sampson,H.A.,

Helm,R.M. and Bannon,G.A.

TITLE

Peanut allergens and methods

JOURNAL

Patent: US 6486311-A 1 26-NOV-2002;

Mc. Sinai School of Medicine and University of Arkansas; New York,

NY

FEATURES

source

1..743 Location/Qualifiers

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/mol_type="genomic DNA"

ORIGIN

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QY	121	GCCTCGAGCAACATCTCATGAGAGATCCACGTCGAGAGGATTCATATGAACGGGA	180		
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QY	181	CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG	240		
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QY	241	ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGATTTGAGAAACAACCAAG	300		
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QY	421	GGCACACAGCGTTGCGACTTGAGAGCTGGAAGTGGGGGAGAGAGATCTAAACACC	480		
Db	426	GGCACACAGCGTTGCGACTTGAGAGCTGGAAGTGGGGGAGAGAGATCTAAACACC	485		
QY	481	TATCTCAAAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTTATATCTATG	540		
Db	486	TATCTCAAAAAAGAAAAGAAAAGAAAAGTCTTATATATAGCTTATATCTATG	545		
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Db	546	GTTATGTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTTA	605		
QY	601	ACTAAGGCAAGCTTAGTTTATAGGACCTTTTAGAGTGCTTTTATGGCGTTGCTATGT	660		
Db	606	ACTAAGGCAAGCTTAGTTTATAGGACCTTTTAGAGTGCTTTTATGGCGTTGCTATGT	665		
QY	661	TTTGTGTCGAGGTTGTAACCATCTTGAATAATATAAAAGATCATGTTTTGTT	717		
Db	666	TTTGTGTCGAGGTTGTAACCATCTTGAATAATATAAAAGATCATGTTTTGTT	722		
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AY722689					
Arachis hypogaea 2S protein 1 mRNA, partial cds.					
AY722689					
AY722689.1 GI:52001226					
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Arachis hypogaea					
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JOURNAL Unpublished
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Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
Direct Submission
TITLE Submitted (01-MAR-2004) Department of Biology and Biotechnology,
School of Life Science, Sun Yat-sen University, Guangzhou,
Guangdong 510275, China
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RNLPQQGLRAPQRCDLEVESGGRDRI"
CDS
Query Match 89.98; Score 644.6; DB 4; Length 842;
Best Local Similarity 93.94; Pred. No. 3.3e-180;
Matches 707; Conservative 0; Mismatches 9; Indels 37; Gaps 2;
QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGTCCGCCACGCATCTCGAGGCA 60
|||||
Db 54 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCTCGTCCGCCACGCATCTCGAGGCA 113
|||||
QY 61 GCAGTGGGAATCTCAAGGACAGAGAAGATCCAGAGCCAGCTCGAGAGGCGGAACCTGAG 120
|||||
Db 114 GCAGTGGGAATCTACNAGGACAGAGAAGATCCAGAGCCAGCTCGAGAGGCGGAACCTTAG 173
|||||
QY 121 GCCTTGGGACACATCTCATGAGAGATCCACGCTGAGAGGATTCATATGACGGGA 180
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Db 174 GCCTTGGGACACATCTCATGAGAGATCCACGCTGAGAGGATTCATATGACGGGA 233
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QY 181 CCCGTACAGCCCTAGTCAG-----GATCC 204
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Db 234 CCCGTACAGCCCTAGTCAGATCGTACAGCCCTAGTCAGAGCCCGGACAGCGTATCC 293
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QY 205 GTACAGCCCTAGTCATATGATCGGAGGCGCTGGATCTCTCAGACCAAGAGAGGTG 264
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Db 294 GTACAGCCCTAGTCATATGATCGGAGGCGCTGGATCTCTCAGACCAAGAGAGGTG 353
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QY 265 TTGCAATGAGCTGAACGAGTTTGGAGAACCAACAAAGGTGCATGTCGAGGCAATTCGAACA 324
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Db 354 TTGCAATGAGCTGAACGAGTTTGGAGAACCAACAAAGGTGCATGTCGAGGCAATTCGAACA 413
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QY 325 GATCATGGAGAACCAAGGAGGATAGTTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAG 384
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Db 414 GATAATGGAGAACCAAGGAGGATAGTTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAG 473
|||||
QY 385 GGAGCTCAGGAACCTTCCTCAACAGTGGCGCTTTAGGGACACACAGCGTTTGGACTTTGGA 444
|||||
Db 474 GGAGCTCAGGAACCTTCCTCAACAGTGGCGCTTCAGGGACACACAGCGTTTGGACTTTGGA 533
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QY 445 CGTCTGAAAGTGGCGGAGACAGATATAACACACCTATCTCAAAAAAGAAAAAGAAAG 504
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Db 534 AGTCGAAAGTGGCGGAGACAGATATAACACACCTATCTCAAAAAAGAAAAAGAAAG 593
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QY 505 AAAAGAAAATAGCTTATATATAAGCTATTATCTATGTTATGTTTGTAGTTTGGTAATAT 564
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Db 594 AAAAGAAAATAGCTTATATATAAGCTATTATCTATGTTATGTTTGTAGTTTGGTAATAT 652
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QY 565 AAAGATCATCATATATGAATGTTGATCGTGTAACTAAAGCAAGCTTTAGGTTATATG 624
|||||
Db 653 AAAGATCATCATATATGAATGTTGATCGTGTAACTAAAGCAAGCTTTAGGTTATATG 712
|||||
QY 625 AGCACCTTTAGAGTGTCTTTATGGCGTGTCTATGTTTGTCTGCAGAGTTGTAAACCA 684
|||||
Db 713 AGCACCTTTAGAGTGTCTTTATGGCGTGTCTATGTTTGTCTGCAGAGTTGTAAACCA 772
|||||
QY 685 TCTTGAATAATAATAAAAGATCATGTTTGT 717
|||||
Db 773 TCTTGAATAATAATAAAAGATCATGTTTGT 805
|||||
RESULT 8
AY581854 678 bp mRNA linear PLN 01-MAY-2004
DEFINITION Arachis hypogaea seed storage protein SSP2 mRNA, partial cds.
ACCESSION AY581854
VERSION AY581854.1 GI:46560481
KEYWORDS Arachis hypogaea (peanut)
SOURCE Arachis hypogaea
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 678)
Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
cDNA cloning of peanut seed storage protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 678)
Yan, Y., Wang, L., Liao, B., Li, H., Lin, X. and Huang, S.
Direct Submission
TITLE Submitted (01-MAR-2004) Department of Biology and Biotechnology,
School of Life Science, Sun Yat-sen University, Guangzhou,
Guangdong 510275, China
FEATURES
source
1..678
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="SanYou523"
/db_xref="taxon:3818"
<1..528
/codon_start=1
/product="seed storage protein SSP2"
/protein_id="AAT00599.1"
/db_xref="GI:46560482"
/translation="DHTLFNTHSIITTTMAKLTILVALALFLAAHASARQOEWELQ
DRRCQSLERANLRPCEQHLMKIQEDSYSDPSPSQDPPSPQDPRDRPPSPS
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RNLPQQGLRAPQRCDLEVESGGRDRI"
CDS
ORIGIN
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Query Match	83.5%;	Score	598.8;	DB	4;	Length	678;		
Best Local Similarity	99.4%;	Pred.	No. 1.4e-166;						
Matches	622;	Conservative	0;	Mismatches	2;	Indels	2;	Gaps	2;

Qy	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGGAGGCA	60
Db	54	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGGAGGCA	113
Qy	61	GCAGTGGGAATCCCAAGGAGACAGAGATGCCAGAGCCAGCTTCGAGAGGGCGAACCTGAG	120
Db	114	GCAGTGGGAATCCCAAGGAGACAGAGATGCCAGAGCCAGCTTCGAGAGGGCGAACCTGAG	173
Qy	121	GCCTCGGAGCAACATCTCATCGAGAGATCCAAAGTACAGAGGATTCATATGACCGGA	180
Db	174	GCCTCGGAGCAACATCTCATCGAGAGATCCAAAGTACAGAGGATTCATATGACCGGA	233
Qy	181	CCCGTACAGCCCTAGTCAGAGTCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTGG	240
Db	234	CCCGTACAGCCCTAGTCAGAGTCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTGG	293
Qy	241	ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACG	300
Db	294	ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACG	353
Qy	301	GTGCATGTCGAGGCAATCCACAGATCATGAGAACAGAGAGGATGTTGAGAGGGGAG	360
Db	354	GTGCATGTCGAGGCAATCCACAGATCATGAGAACAGAGAGGATGTTGAGAGGGGAG	413
Qy	361	GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACTTTCCTCAACAGTTCGCGCTTAG	420
Db	414	GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACTTTCCTCAACAGTTCGCGCTTAG	473
Qy	421	GGCACCACAGCTTGGCACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	480
Db	474	GGCACCACAGCTTGGCACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	533
Qy	481	TATCTCAAAAAG	539
Db	534	TATCTCAAAAAG	593
Qy	540	GGTATGTTTGGTAAATTAAGATCATCACTATATGAATGTTGATCGTGT	599
Db	594	GGTATGTTTGGTAAATTAAGATCATCACTATATGAATGTTGATCGTGT	652
Qy	600	AACAGGCAAGCTTAGTTATATGA	625
Db	653	AACAGGCAAGCTTAGTTATATGA	678

RESULT 9	BD107899	474 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD107899	474 bp	DNA	linear	PAT 18-SEP-2002
DEFINITION	Methods and reagents for decreasing allergic reactions.				
ACCESSION	BD107899				
VERSION	BD107899.1	GI:23202717			
KEYWORDS	JP 2002501748-A/2.				
SOURCE	unidentified				
ORGANISM	unclassified sequences.				
REFERENCE	1 (bases 1 to 474)				
AUTHORS	Sosin, H., Banon, G.A., Jr, W.A.B. and Sampthson, H.A.				
TITLE	Methods and reagents for decreasing allergic reactions				
JOURNAL	Patent: JP 2002501748-A 2 22-JAN-2002;				
	UNIVERSITY OF ARKANSAS, MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY				
	UNIVERSITY OF NEW YORK, HOWARD SOSIN				
COMMENT	OS Arachis L. (Peanut)				
	PN JP 2002501748-A/2				
	PD 22-JAN-1999				
	PR 29-JAN-1998				
	PF 31-JAN-1998				
	13-FEB-1998				
	27-AUG-1998				

Query Match	83.5%;	Score	598.8;	DB	4;	Length	678;		
Best Local Similarity	99.4%;	Pred.	No. 1.4e-166;						
Matches	622;	Conservative	0;	Mismatches	2;	Indels	2;	Gaps	2;

Qy	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGGAGGCA	60
Db	54	GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTGGAGGCA	113
Qy	61	GCAGTGGGAATCCCAAGGAGACAGAGATGCCAGAGCCAGCTTCGAGAGGGCGAACCTGAG	120
Db	114	GCAGTGGGAATCCCAAGGAGACAGAGATGCCAGAGCCAGCTTCGAGAGGGCGAACCTGAG	173
Qy	121	GCCTCGGAGCAACATCTCATCGAGAGATCCAAAGTACAGAGGATTCATATGACCGGA	180
Db	174	GCCTCGGAGCAACATCTCATCGAGAGATCCAAAGTACAGAGGATTCATATGACCGGA	233
Qy	181	CCCGTACAGCCCTAGTCAGAGTCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTGG	240
Db	234	CCCGTACAGCCCTAGTCAGAGTCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTGG	293
Qy	241	ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACG	300
Db	294	ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACAAACG	353
Qy	301	GTGCATGTCGAGGCAATCCACAGATCATGAGAACAGAGAGGATGTTGAGAGGGGAG	360
Db	354	GTGCATGTCGAGGCAATCCACAGATCATGAGAACAGAGAGGATGTTGAGAGGGGAG	413
Qy	361	GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACTTTCCTCAACAGTTCGCGCTTAG	420
Db	414	GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACTTTCCTCAACAGTTCGCGCTTAG	473
Qy	421	GGCACCACAGCTTGGCACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	480
Db	474	GGCACCACAGCTTGGCACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	533
Qy	481	TATCTCAAAAAG	539
Db	534	TATCTCAAAAAG	593
Qy	540	GGTATGTTTGGTAAATTAAGATCATCACTATATGAATGTTGATCGTGT	599
Db	594	GGTATGTTTGGTAAATTAAGATCATCACTATATGAATGTTGATCGTGT	652
Qy	600	AACAGGCAAGCTTAGTTATATGA	625
Db	653	AACAGGCAAGCTTAGTTATATGA	678

RESULT 10	AX155333	474 bp	DNA	linear	PAT 22-JUN-2001
LOCUS	AX155333	474 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION					

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FEATURES
  source      Location/Qualifiers
            1..474
            /organism="Arachis hypogaea"
            /mol_type="unassigned DNA"
            /db_xref="taxon:3818"

ORIGIN
Query Match      65.9%; Score 472.4; DB 2; Length 474;
Best Local Similarity 99.8%; Pred. No. 5.5e-129;
Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  CTACCACTACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTGGAGGCGAG 61
    |||
Db  1  CTACCACTACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTGGAGGCGAG 60

Qy  62  CAGTGGGAATCTCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 121
    |||
Db  61  CAGTGGGAATCTCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 120

Qy  122  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 181
    |||
Db  121  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 180

Qy  182  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 241
    |||
Db  181  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 240

Qy  242  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 301
    |||
Db  241  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 300

Qy  302  TGCATGTGCCAGGCAATTCGAACAGATCATGAGAACAGAGCGATAGTTTGCAGGGGAGG 361
    |||
Db  301  TGCATGTGCCAGGCAATTCGAACAGATCATGAGAACAGAGCGATAGTTTGCAGGGGAGG 360

Qy  362  CAACAGAGCAACAGTTCAAGAGGAGCTCAGGAATTGCTCAACAGTCGCGCTTAGG 421
    |||
Db  361  CAACAGAGCAACAGTTCAAGAGGAGCTCAGGAATTGCTCAACAGTCGCGCTTAGG 420

Qy  422  GCACCACAGGCTTGGAGCTTGGAGCTGAAAGTGGCGGCGAGACAGACATATA 475
    |||
Db  421  GCACCACAGGCTTGGAGCTTGGAGCTGAAAGTGGCGGCGAGACAGACATATA 474

RESULT 11
BD172108
LOCUS      BD172108 Peanut allergen and method. 474 bp DNA linear PAT 18-FEB-2003
DEFINITION Peanut allergen and method.
ACCESSION BD172108
VERSION    BD172108.1 GI:28413406
KEYWORDS   JP 200223783-A/1.
SOURCE     Arachis hypogaea (peanut)
ORGANISM   Arachis hypogaea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
            Aeschynomeneae; Arachis.
            1 (bases 1 to 474)
REFERENCE  1
AUTHORS    Jt,W.A.B., Helm,R.M., Cockrell,G., Steven, Stanley,J. and
            Bannon,G.A.
TITLE      Peanut allergen and method
JOURNAL    UNIVERSITY OF ARKANSAS
COMMENT    OS Arachis hypogaea (peanut)
            PN JP 200223783-A/1
            PD 13-AUG-2002
            PF 21-NOV-2001 JP 2001356754
            PR 29-DEC-1995 US 60/009 455, 04-MAR-1996 US 08/610 424 PI
            WESLEY A BURNS JR,RICKI M HELM,GARL COCKRELL,STEVEN PI J
            STANLEY,GARY A BANNON
            PC C12N15/09,A61K38/00,A61P37/04,C07K14/415,C12N15/00,A61K37/02
            CC Strandedness: Double;
            Topology: Linear;

FEATURES
  source      Location/Qualifiers
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            /organism="Arachis hypogaea"
            /mol_type="genomic DNA"
            /db_xref="taxon:3818"

ORIGIN
Query Match      65.7%; Score 470.8; DB 2; Length 474;
Best Local Similarity 99.6%; Pred. No. 1.7e-128;
Matches 472; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  CTACCACTACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTGGAGGCGAG 61
    |||
Db  1  CTACCACTACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTGGAGGCGAG 60

Qy  62  CAGTGGGAATCTCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 121
    |||
Db  61  CAGTGGGAATCTCCAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCCTGAGG 120

Qy  122  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 181
    |||
Db  121  CCCTGCCAGCAACATCTCATGCAGAAATCCAACTGACGAGGATTCATATGAACGGGAC 180

Qy  182  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 241
    |||
Db  181  CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTTGA 240

Qy  242  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 301
    |||
Db  241  TCCTCTCAGCACCAGAGAGGTGTGCAATGAGCTGAACGATTTGAGAACCAACCAAGG 300

Qy  302  TGCATGTGCCAGGCAATTCGAACAGATCATGAGAACAGAGCGATAGTTTGCAGGGGAGG 361
    |||
Db  301  TGCATGTGCCAGGCAATTCGAACAGATCATGAGAACAGAGCGATAGTTTGCAGGGGAGG 360

Qy  362  CAACAGAGCAACAGTTCAAGAGGAGCTCAGGAATTGCTCAACAGTCGCGCTTAGG 421
    |||
Db  361  CAACAGAGCAACAGTTCAAGAGGAGCTCAGGAATTGCTCAACAGTCGCGCTTAGG 420

Qy  422  GCACCACAGGCTTGGAGCTTGGAGCTGAAAGTGGCGGCGAGACAGACATATA 475
    |||
Db  421  GCACCACAGGCTTGGAGCTTGGAGCTGAAAGTGGCGGCGAGACAGACATATA 474

RESULT 12
AY007229
LOCUS      AY007229 Arachis hypogaea allergen II gene, partial cds. 472 bp DNA linear PLN 23-OCT-2002
DEFINITION Arachis hypogaea allergen II gene, partial cds.
ACCESSION AY007229
VERSION    AY007229.1 GI:15418704
KEYWORDS   J. Allergy Clin. Immunol. 107 (4), 713-717 (2001)
SOURCE     Arachis hypogaea (peanut)
ORGANISM   Arachis hypogaea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
            Aeschynomeneae; Arachis.
            1 (bases 1 to 472)
REFERENCE  1
AUTHORS    Viquez,O.M., Summer,C.G. and Dodo,H.W.
            Isolation and molecular characterization of the first genomic clone
            of a major peanut allergen, Ara h 2
            J. Allergy Clin. Immunol. 107 (4), 713-717 (2001)
            11295663
            2 (bases 1 to 472)
REFERENCE  2
AUTHORS    Viquez,O.M., Dodo,H.W. and Summer,C.G.
            Direct Submission
            Submitted (16-AUG-2000) Food and Animal Sciences, Alabama A&M
            University, Meridian Street, 4900, Normal, AL 35762, USA
            Location/Qualifiers
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CDS         3..>.472
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ORIGIN
Query Match      64.4%; Score 462; DB 4; Length 472;
Best Local Similarity 100.0%; Pred. No. 6.9e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 60
DB      11 GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 70
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 120
DB      71 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 130
QY      121 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 180
DB      131 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 190
QY      181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 240
DB      191 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 250
QY      241 ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACAAAG 300
DB      251 ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACAAAG 310
QY      301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGTTTGCAGGGGAG 360
DB      311 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGTTTGCAGGGGAG 370
QY      361 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 420
DB      371 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 430
QY      421 GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAG 462
DB      431 GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAG 472

RESULT 13
AR716327 LOCUS      682 bp      DNA      linear      PAT 07-OCT-2005
DEFINITION Sequence 3 from patent US 6943010.
ACCESSION AR716327
VERSION AR716327.1 GI:77364702
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 682)
Dodo,H.W., Arntzen,C.J., Viquez,O.M. and Konan,K.N.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: US 6943010-A 3 13-SEP-2005;
FEATURES
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1. .682
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      64.4%; Score 462; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 60
DB      67 GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 126
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 120
DB      127 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 186
QY      121 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 180
DB      187 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 246
QY      181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 240
DB      247 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 306
QY      241 ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACAAAG 300
DB      307 ATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACAAAG 366
QY      301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGTTTGCAGGGGAG 360
DB      367 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACCAAGAGCGATAGTTTGCAGGGGAG 426
QY      361 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 420
DB      427 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 486
QY      421 GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAG 462
DB      487 GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAG 528

RESULT 14
AX148740 LOCUS      682 bp      DNA      linear      PAT 08-JUN-2001
DEFINITION Sequence 3 from Patent WO0136621.
ACCESSION AX148740
VERSION AX148740.1 GI:14347294
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Dodo,H.W., Arntzen,C.J., Konan,K.N. and Viquez,O.M.
TITLE Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: WO 0136621-A 3 25-MAY-2001;
FEATURES
source
1. .682
/organism="Arachis hypogaea"
/mol_type="unassigned DNA"
/db_xref="taxon:3818"

ORIGIN
Query Match      64.4%; Score 462; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 7.3e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 60
DB      67 GCTCACCATACTAGTACCCCTCGCCCTTTTCTCCTCGCTGCCCGCCGCAATCTCGGAGGCA 126
QY      61 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 120
DB      127 GCAGTGGGAACCTCAAGGACACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCTAG 186
QY      121 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 180
DB      187 GCCTTCGAGCAACATCTCATGCAGAGATCCAAAGCTGACGAGGATTCATATGAACGGGA 246
QY      181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 240
DB      247 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGAGCGCTGG 306
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QY      361 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 420
DB      427 GCAACAGGAGCAACAGTTCGAAGAGGGAGCTCAGAACTTCCTTCAACAGTTCGCGCCCTTAG 486
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Db 247 CCCGTACAGCCCTAGTTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 306
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Db 307 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACCAAAAG 366
Qy 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGCCAGAGCCAGAGCCATAGTTGCAAGGGAG 360
Db 367 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGCCAGAGCCATAGTTGCAAGGGAG 426
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Db 487 GGCACCAACAGCTTGGACCTTGGACCTCGAAAGTGGCGGCAG 528
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RESULT 15

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AR716326
LOCUS AR716326 1162 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 1 from patent US 6943010.
ACCESSION AR716326
VERSION AR716326.1 GI:77364701
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1162)
Dodo,H.W., Arntzen,C.J., Viquez O.M. and Konan,K.N.
Down-regulation and silencing of allergen genes in transgenic
peanut seeds
JOURNAL Patent: US 6943010-A 1 13-SEP-2005;
FEATURES
source
1. 1162
/organism="unknown"
/mol_type="genomic DNA"
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ORIGIN

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Query Match 64.4%; Score 462; DB 2; Length 1162;
Best Local Similarity 100.0%; Pred. No. 7.9e-126;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTCGAGGCA 60
Db 118 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCAATCTCGAGGCA 177
Qy 61 GCAGTGGGAACCTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGGGCGAAACCTGAG 120
Db 178 GCAGTGGGAACCTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGGGCGAAACCTGAG 237
Qy 121 GCCCTGGGAGCAACATCTCATGCAAGAGATCCAAAGCTGACGAGATTCATATGAACGGGA 180
Db 238 GCCCTGGGAGCAACATCTCATGCAAGAGATCCAAAGCTGACGAGATTCATATGAACGGGA 297
Qy 181 CCCGTACAGCCCTAGTTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240
Db 298 CCCGTACAGCCCTAGTTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 357
Qy 241 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACCAAAAG 300
Db 358 ATCTCTCAGACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAAACCAAAAG 417
```

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Qy 301 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACAGAGCGATAGTTGCAAGGGAG 360
Db 418 GTGCATGTGCGAGGCATTGCAACAGATCATGGAGAACAGAGCGATAGTTGCAAGGGAG 477
Qy 361 GCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACTTGCCTCAACAGTGGCGCCTTAG 420
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Qy 421 GGCACCAACAGCTTGGACCTTGGACCTCGAAAGTGGCGGCAG 462
Db 538 GGCACCAACAGCTTGGACCTTGGACCTCGAAAGTGGCGGCAG 579
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Search completed: June 23, 2006, 18:12:45
Job time : 4186.37 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2006, 09:14:45 ; Search time 319.487 Seconds
(without alignments)

15647.278 Million cell updates/sec

Title: US-10-728-051-2

Perfect score: 717

Sequence: 1 gccaccatactagtagcc.....taaaagatcatgtttgtt 717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_8.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
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- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
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- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*
- 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	717	100.0	717	2 AAT76615	Aat76615 Peanut al
2	717	100.0	717	2 AAT76614	Aat76614 Peanut al
3	717	100.0	717	14 ADV97538	Adv97538 Peanut Ar
4	717	100.0	717	14 ADV97541	Adv97541 Peanut Ar
5	475	66.2	480	14 ADV97602	Adv97602 Peanut Ar
6	474	66.1	474	2 AAZ06383	Aaz06383 Peanut al
7	474	66.1	474	4 AAS08538	Aas08538 DNA encod
8	474	66.1	474	8 ABX70606	Abx70606 Peanut Ar
9	474	66.1	474	10 ADG27517	Adg27517 Peanutur CD
10	462	64.4	682	4 AAF90337	Aaf90337 Peanut al
11	462	64.4	1162	4 AAF90336	Aaf90336 Peanut al
12	80	11.2	80	4 AAF90342	Aaf90342 Peanut al
13	65.6	9.1	777	2 AAT86282	Aat86282 Soybean a
14	64	8.9	777	2 AAT86283	Aat86283 Chimeric
15	63.4	8.8	770	2 AAX25345	Aax25345 Soybean G
16	62	8.6	62	4 AAF90343	Aaf90343 Peanut al
17	59.2	8.3	477	10 ADH89268	Adh89268 G. max 2S
18	59.2	8.3	477	12 ADG44003	Adg44003 G. max 2S

19	54.4	7.6	468	10	ADH89266	Adh89266 G. max na
20	54.4	7.6	468	12	ADG44001	Adg44001 G. max 2S
21	54.4	7.6	723	2	AAT86281	Aat86281 Soybean a
22	51.4	7.2	5392	2	AZ08720	Az08720 Chimeric
C 23	49.8	6.9	62658	13	ABD33339	Abd33339 Human can
C 24	49.6	6.9	52216	4	AAH28355	Aah28355 Nucleotid
C 25	49.6	6.9	52216	6	ABL50307	AbL50307 Human mus
C 26	49.6	6.9	169739	6	ABQ88186	Abq88186 Human ost
27	49	6.8	129	4	AAF87134	Aaf87134 Lusanin c
28	49	6.8	129	4	AAF83653	Aaf83653 Soybean c
29	49	6.8	9407	4	AAF83654	Aaf83654 pPIC9K-lu
30	49	6.8	9408	4	AAF87135	Aaf87135 Lusanin c
31	48.2	6.7	7758	6	ABL33103	AbL33103 Human imm
32	48	6.7	6509	6	ABL32226	AbL32226 Human imm
33	47.4	6.6	97835	6	ABK84796	Abk84796 Human cDN
34	45.6	6.4	2000	8	ADA71938	Ada71938 Rice gene
35	45.6	6.4	6063	6	ABK28393	Abk28393 DNA trans
C 36	45.4	6.3	5823	6	ABK28382	Abk28382 DNA trans
37	45.2	6.3	121724	6	ABQ88143	Abq88143 Human ost
38	44.8	6.2	20001	13	ADT77147	Adt77147 Type II d
39	44.4	6.2	6050	10	ADE84181	Ade84181 Human lym
C 40	44.4	6.2	6385	4	AAS45353	Aas45353 Chemicall
C 41	44.4	6.2	6385	6	ABK28186	Abk28186 DNA trans
42	44.4	6.2	110000	2	AAV21209_04	Continuation (5 of
43	44	6.1	608	6	ABNG2524	Abng2524 Human can
44	44	6.1	608	14	ACL60109	ACL60109 Human col
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ALIGNMENTS

RESULT 1

AAT76615
ID AAT76615 standard; cDNA to mRNA; 717 BP.

AC AAT76615;

DT 17-OCT-2003 (revised)

DT 29-DEC-1997 (first entry)

DE Peanut allergen Ara hII cDNA clone.

KW Peanut; seed storage protein; allergen; allergy; hypersensitivity;

KW vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;

KW ELISA; analysis; Ara hII; ds.

OS Arachis hypogaea; strain Florunner.

FH Key Location/Qualifiers

CDS 2..475

FT /*tag= a

FT polyA_signal 562..567

FT /*tag= b

XX WO9724139-A1.

PD 10-JUL-1997.

PF 23-SEP-1996; 96WO-US015222.

PR 29-DEC-1995; 95US-0009455P.

PR 04-MAR-1996; 96US-00610424.

XX (UYAR-) UNIV ARKANSAS.

XX Burks AW, Helm RM, Cockrell G, Stanley JS, Bannon GA;

XX WPI; 1997-363453/33.

DR P-PSDB; AAW24153.

XX Peanut allergens Ara hI and Ara hII - used for vaccination and in two-

PT site monoclonal antibody based ELISA.

XX Claim 31; Page 196; 354pp; English.

PS This cDNA clone codes for the major peanut allergen Ara hII (AAW22153),

XX which contains multiple IgE-binding epitopes. It was amplified from a

CC peanut seed cDNA library using a primer (see AAT58683) based on an

CC isolated Ara hII peptide (see AAW24151). The sequence shows significant

CC homology with the conglutin family of seed storage proteins of other

CC legumes. The gene is capable of producing a protein product in

CC prokaryotic cells that is recognised by serum IgE from a large proportion

CC of individuals with peanut hypersensitivity. Ara hII and Ara hI (see

CC AAW24149-50) can be used to raise monoclonal antibodies which are used in

CC a specific two-site Mab ELISA for the detection of Ara hI or Ara hII

CC (claimed). IgE-binding Ara hII antigen epitopes (see AAW24188- 93) may be

CC used in vaccines to protect against allergic reactions to peanut

CC allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to

CC standardise OS field)

XX Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 717; DB 2; Length 717;

Best Local Similarity 100.0%; Pred. No. 7e-178;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGCATCTCGGAGGCA 60

DB |||||

QY 61 GCAGTGGGAACCTCAAGGAGACAGAGAATGCCAGAGCCAGCTCGAGGGCGCAACCTTGAG 120

DB |||||

QY 61 GCAGTGGGAACCTCAAGGAGACAGAGAATGCCAGAGCCAGCTCGAGGGCGCAACCTTGAG 120

DB |||||

QY 121 GCCCTCGAGCAACATCTCATGAGAGATGCCAAGATGCCAAGTTCATATGAACGGGA 180

DB |||||

QY 121 GCCCTCGAGCAACATCTCATGAGAGATGCCAAGTTCATATGAACGGGA 180

DB |||||

QY 181 CCCGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCCTATATGATCGGAGGCCCTGG 240

DB |||||

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QY 241 ATCCTCTCAGCACACAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300

DB |||||

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DB |||||

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DB |||||

QY 301 GTGCATGTGCGAGGCAATGCAACAGATCATGGAACACAGAGCGATAGTTGACAGGGAG 360

DB |||||

QY 361 GCAACAGGACACAGTTCAGAGGGAGCTCAGGAACCTTCCTCAACAGTGGCGCCTTAG 420

DB |||||

QY 361 GCAACAGGACACAGTTCAGAGGGAGCTCAGGAACCTTCCTCAACAGTGGCGCCTTAG 420

DB |||||

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DB |||||

QY 421 GGCAACACACAGCTTGCAGCTTGCAAGTGGGAGTGGCGGCGAGACAGATACCTAAACACC 480

DB |||||

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DB |||||

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DB |||||

QY 541 GTTATGTTTATGTTTGGTAAATAAAGATCATCATATATGATGTTGATCGTGTAA 600

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DB |||||

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DB |||||

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DB |||||

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DB |||||

RESULT 2

AAAT76614

ID AAT76614 standard; cDNA to mRNA; 717 BP.

XX

AC AAT76614;

XX

DT 17-OCT-2003 (revised)

DT 29-DEC-1997 (first entry)

XX

DE Peanut allergen Ara hII cDNA clone P38.

XX

KW Peanut; seed storage protein; allergen; allergy; hypersensitivity;

KW vaccine; anaphylactic shock; immunotherapy; therapy; monoclonal antibody;

KW ELISA; analysis; Ara hII; ds.

XX

OS Arachis hypogaea; strain Florunner.

XX

FH Key Location/Qualifiers

FT CDS 2..475

FT polyA_signal /*tag= a

FT /*tag= b

XX

PN WO9724139-A1.

XX

PD 10-JUL-1997.

XX

PF 23-SEP-1996; 96WO-US015222.

XX

PR 29-DEC-1995; 95US-0009455P.

PR 04-MAR-1996; 96US-00610424.

XX

PA (UYAR-) UNIV ARKANSAS.

XX

PI Burks AW, Helm RM, Cockrell G, Stanley JS, Bannon GA;

XX

DR WPI; 1997-363453/33.

XX

PT Peanut allergens Ara hI and Ara hII - used for vaccination and in two-site monoclonal antibody based ELISA.

XX

PS Claim 31; Page 183-185; 354pp; English.

XX

CC This cDNA clone, designated p38, codes for the major peanut allergen Ara hII (AAW22153), which contains multiple IgE-binding epitopes. It was amplified from a peanut seed cDNA library using a primer (see AAT58683) based on an isolated Ara hII peptide (see AAW24151). The sequence shows significant homology with the conglutin family of seed storage proteins of other legumes. The gene is capable of producing a protein product in prokaryotic cells that is recognised by serum IgE from a large proportion of individuals with peanut hypersensitivity. Ara hII and Ara hI (see AAW24149-50) can be used to raise monoclonal antibodies which are used in a specific two-site Mab ELISA for the detection of Ara hI or Ara hII (claimed). IgE-binding Ara hII antigen epitopes (see AAW24188- 93) may be used in vaccines to protect against allergic reactions to peanut allergens, e.g. anaphylactic shock. (Updated on 17-OCT-2003 to standardise OS field)

XX

SQ Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;

Query Match 100.0%; Score 717; DB 2; Length 717;

Best Local Similarity 100.0%; Pred. No. 7e-178;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGCATCTCGGAGGCA 60

DB |||||

QY 1 GCAGTGGGAACCTCAAGGAGACAGAGAATGCCAGAGCCAGCTCGAGGGCGCAACCTTGAG 120

DB |||||

QY 61 GCAGTGGGAACCTCAAGGAGACAGAGAATGCCAGAGCCAGCTCGAGGGCGCAACCTTGAG 120

DB |||||

QY 121 GCCCTCGAGCAACATCTCATGAGAGATGCCAAGATGCCAAGTTCATATGAACGGGA 180

DB |||||

Db 121 GCGCTGGGCAACATCTCTCATGCAAGAGATCCAAACGTCGACAGAGATTCATATGAACGGGA 180
Qy 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
Db 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
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Db 301 GTGCATGTGGAGGCAATTCGAACAGATCATGGAGAACCAAGCGATAGGTTGCGAGGGAG 360
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Db 601 ACTAAGCAAGCTTAGTTTATATGAGCAACCTTTAGAGTGCTTTTATGCGGTGCTATGT 660
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Db 661 TTTGTTGCTGAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGCTTTTGT 717

RESULT 3
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ID ADV97538 standard; cDNA; 717 BP.
XX
AC ADV97538;
XX
DT 10-MAR-2005 (first entry)
XX
DE Peanut Ara h II allergen clone P38 cDNA encoding a seed storage protein.
XX
KW allergen; atopic dermatitis; diagnostic; immunotherapy;
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;
KW immunosuppressive; antibody engineering; ss; gene.
XX
OS Arachis hypogaea.
XX
FH Key Location/Qualifiers
FT CDS 2..475
FT /*tag= a
FT /partial
FT /product= "Ara h II protein"
FT /note= "Start codon is absent"
XX
XX US6835824-B1.
XX
XX 28-DEC-2004.
XX
XX 13-NOV-1998; 98US-00191593.
XX
XX 29-DEC-1995; 95US-0009455P.
XX
XX 23-SEP-1996; 96US-00717933.
XX
XX (UYAR-) UNIV ARKANSAS.
PA

XX Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX WPI: 2005-045982/05.
XX P-PSDB; ADV97542.
XX
XX New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
XX obtaining diagnostics with optimal concentrations of each allergen, for
XX developing panels of mixtures of recombinant allergens, and in
XX immunotherapy.
XX
XX Disclosure; SEQ ID NO 6; 141pp; English.
XX
XX This invention relates to a novel isolated nucleic acid molecule encoding
XX the peanut allergen Ara h I that has been identified in patients with
XX atopic dermatitis. Specifically, it refers to a monoclonal antibody
XX enzyme-linked immunosorbent assay (ELISA) used to detect and quantify the
XX peanut allergens, where the monoclonal antibodies have specificity for a
XX selected peanut allergen antigen. The present invention also describes
XX hybridomas that produce two-site monoclonal antibodies specific for a
XX peanut allergen that can be used in an ELISA to detect and determine the
XX concentration of a specific peanut allergen in a food product or in food
XX processing. Furthermore, it provides an expression vector and the
XX isolated nucleic acid or its fraction can include a diagnostic label.
XX Accordingly, these nucleic acids are useful for obtaining diagnostics
XX with optimal concentrations of each allergen or for developing panels of
XX mixtures of large numbers of recombinant allergens such that it can be
XX used in immunotherapy for the treatment of food hypersensitivity
XX reactions. This polynucleotide sequence is the peanut Ara h II allergen
XX cDNA (P38 clone) of the invention. NB. This sequence is identical to that
XX identified as SeqID 9.
XX
XX Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;
Query Match 100.0%; Score 717; DB 14; Length 717;
Best Local Similarity 100.0%; Pred. No. 7e-178;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCATCTGCGAGGCA 60
Db 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACGCATCTGCGAGGCA 60
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Db 61 GCAGTGGGAACTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGCGAACCCTGAG 120
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Db 121 GCCCTCGAGCAACATCTCATGCGAGAGATCCAAACGTGACGAGATTTCATATGAACGGGA 180
Qy 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
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DB |||||||
QY 541 GTTATGTTAGTTTGGTAATAATAAAGATCATCACTATATGAATGTGTGATCGTGTTA 600
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QY 601 ACTAAGCGCAGCTAGTTATATAGCACCTTTAGAGTGTCTTTATGCGGTTGCTATGT 660
DB |||||||
QY 601 ACTAAGCGCAGCTAGTTATATAGCACCTTTAGAGTGTCTTTATGCGGTTGCTATGT 660
DB |||||||
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTGT 717
DB |||||||
661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTGT 717
RESULT 4
ADV97541
ID ADV97541 standard; cDNA; 717 BP.
XX
AC ADV97541;
XX
10-MAR-2005 (first entry)
XX
DT Peanut Ara h II allergen clone p38 cDNA encoding a seed storage protein.
XX
DE allergen; atopic dermatitis; diagnostic; immunotherapy;
XX
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;
KW immunosuppressive; antibody engineering; ss.
XX
OS Arachis hypogaea.
XX
FH Key Location/Qualifiers
FT CDS 2..475
FT /*tag= a
FT /partial
FT /product= "Ara h II protein"
FT /note= "Start codon is absent"
XX
US6835824-B1.
XX
28-DEC-2004.
XX
13-NOV-1998; 98US-00191593.
XX
29-DEC-1995; 95US-0009455P.
PR 23-SEP-1996; 96US-00717933.
XX
(UVAR-) UNIV ARKANSAS.
XX
PI Burks AW, Stanley JS, Bannon GA, Cockrell G, Helm RM;
XX
WPI; 2005-045982/05.
DR P-PSDB; ADV97542.
XX
PT New isolated nucleic acid encoding peanut allergen Ara h 1, useful for
XX obtaining diagnostics with optimal concentrations of each allergen, for
PT developing panels of mixtures of recombinant allergens, and in
PT immunotherapy.
XX
PS Disclosure; SEQ ID NO 9; 141pp; English.
XX
CC This invention relates to a novel isolated nucleic acid molecule encoding
CC the peanut allergen Ara h I that has been identified in patients with
CC atopic dermatitis. Specifically, it refers to a monoclonal antibody
CC enzyme-linked immunosorbant assay (ELISA) used to detect and quantify the
CC peanut allergens, where the monoclonal antibodies have specificity for a
CC selected peanut allergen antigen. The present invention also describes
CC hybridomas that produce two-site monoclonal antibodies specific for a
CC peanut allergen that can be used in an ELISA to detect and determine the
CC concentration of a specific peanut allergen in a food product or in food
CC processing. Furthermore, it provides an expression vector and the
CC isolated nucleic acid or its fraction can include a diagnostic label.
CC Accordingly, these nucleic acids are useful for obtaining diagnostics
CC with optimal concentrations of each allergen or for developing panels of

CC mixtures of large numbers of recombinant allergens such that it can be
CC used in immunotherapy for the treatment of food hypersensitivity
CC reactions. This polynucleotide sequence is the peanut Ara h II allergen
CC cDNA (P38 clone) of the invention. NB. This sequence is identical to that
CC identified as SeqID 6.
XX
SQ Sequence 717 BP; 217 A; 152 C; 184 G; 164 T; 0 U; 0 Other;
Query Match 100.0%; Score 717; DB 14; Length 717;
Best Local Similarity 100.0%; Pred. No. 7e-178;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCACCTACTAGTAGCCCTGCGCCCTTTTCTCTCTCGTCCCGCAGCATCTCGAGGCA 60
DB |||||||
1 GCTCACCTACTAGTAGCCCTGCGCCCTTTTCTCTCTCGTCCCGCAGCATCTCGAGGCA 60
DB |||||||
QY 61 GCAGTGGGAATCTCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACTGAG 120
DB |||||||
61 GCAGTGGGAATCTCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACTGAG 120
DB |||||||
QY 121 GCCCTGGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA 180
DB |||||||
121 GCCCTGGAGCAACATCTCATGCAGAAAGATCCAACTGACGAGGATTCATATGAACGGGA 180
DB |||||||
QY 181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240
DB |||||||
181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240
DB |||||||
QY 241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAAGCTTTTGAGAACCAACAAAG 300
DB |||||||
241 ATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAAGCTTTTGAGAACCAACAAAG 300
DB |||||||
QY 301 GTGCATGTGCGAGGCAATTGCAACAGATCATGGAACACGAGCGATAGTTGCGAGGGAG 360
DB |||||||
301 GTGCATGTGCGAGGCAATTGCAACAGATCATGGAACACGAGCGATAGTTGCGAGGGAG 360
DB |||||||
QY 361 GCAACAGGAGCAACAGTTCAGAGAGGAGCTCAGGAACTTGCTCAACAGTGGCGCTTAG 420
DB |||||||
361 GCAACAGGAGCAACAGTTCAGAGAGGAGCTCAGGAACTTGCTCAACAGTGGCGCTTAG 420
DB |||||||
QY 421 GGCACCAACAGCGTTGCGACTTGACAGCTCGAAAGTGGCGGAGAGACAGATACATAACACC 480
DB |||||||
421 GGCACCAACAGCGTTGCGACTTGACAGCTCGAAAGTGGCGGAGAGACAGATACATAACACC 480
DB |||||||
QY 481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
DB |||||||
481 TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
DB |||||||
QY 541 GTTATGTTAGTTTGGTAATAATAAAGATCATCACTATATGAATGTGTGATCGTGTTA 600
DB |||||||
541 GTTATGTTAGTTTGGTAATAATAAAGATCATCACTATATGAATGTGTGATCGTGTTA 600
DB |||||||
QY 601 ACTAAGCGCAGCTAGTTATATGAGCACCTTTAGAGTGTCTTTATGCGGTTGCTATGT 660
DB |||||||
601 ACTAAGCGCAGCTAGTTATATGAGCACCTTTAGAGTGTCTTTATGCGGTTGCTATGT 660
DB |||||||
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTGT 717
DB |||||||
661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATAATAAAGATCATGTTTGT 717
RESULT 5
ADV97602
ID ADV97602 standard; cDNA; 480 BP.
XX
AC ADV97602;
XX
DT 10-MAR-2005 (first entry)
XX
DE Peanut Ara h II allergen clone p38 cDNA encoding a seed storage protein.
XX
KW allergen; atopic dermatitis; diagnostic; immunotherapy;
KW immediate type hypersensitivity; Ara h II; dermatological; antiallergic;

Matches	474;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCAG	61						
Db	1	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCATCTCGAGGCAG	60						
Qy	62	CAGTGGGAACCTCCAAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCAGG	121						
Db	61	CAGTGGGAACCTCCAAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCAGG	120						
Qy	122	CCCTGCGAGCAACATCTCATGCGAAGAATCCAAAGTGCAGGAGATTCATATGAACGGGAC	181						
Db	121	CCCTGCGAGCAACATCTCATGCGAAGAATCCAAAGTGCAGGAGATTCATATGAACGGGAC	180						
Qy	182	CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGGA	241						
Db	181	CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGGA	240						
Qy	242	TCCTCTCAGCACCAAGAGAGGTGTGCAATCAGCTGACGAGTTTGAGAACCAACAAAGG	301						
Db	241	TCCTCTCAGCACCAAGAGAGGTGTGCAATCAGCTGACGAGTTTGAGAACCAACAAAGG	300						
Qy	302	TGCATGTGCGAGGATTGCAACAGATCATGAGAACCCAGACCGATAGGTTTCAGGGGAGG	361						
Db	301	TGCATGTGCGAGGATTGCAACAGATCATGAGAACCCAGACCGATAGGTTTCAGGGGAGG	360						
Qy	362	CAACAGAGCAACAGTTTCAACAGGGAGCTCAGGAACTTGGCTCAACAGTCGGCGCTTAGG	421						
Db	361	CAACAGAGCAACAGTTTCAACAGGGAGCTCAGGAACTTGGCTCAACAGTCGGCGCTTAGG	420						
Qy	422	GCACCAAGCGTTGCGACTTGGACGTCGAAAGTCGGCGGACAGACAGATACTAA	475						
Db	421	GCACCAAGCGTTGCGACTTGGACGTCGAAAGTCGGCGGACAGACAGATACTAA	474						

RESULT 7
AAS08538
ID AAS08538 standard; cDNA; 474 BP.
XX
XX AAS08538;
XX
XX
XX
DT 23-OCT-2001 (first entry)
XX
XX DNA encoding anaphylactic antigen Ara h 2.
DE
XX
XX Ara h 2; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;
KW allergen; mast cell; basophil; mouse; ss.

Key	Location/Qualifiers
XX	
PH	1. .474
FT	/*tag= a
FT	/product= "peptide antigen Ara h 2"
FT	
XX	
XX	WO200140264-A2.
PN	
XX	
XX	
PD	07-JUN-2001.
XX	
PF	06-DEC-2000; 2000WO-US033124.
PF	
XX	
PR	06-DEC-1999; 99US-00455294.
PR	23-JUN-2000; 2000US-0213785P.
PR	27-SEP-2000; 2000US-0235797P.
PR	

XX Antigenic fragments useful for reducing anaphylactic risk and reducing
PT the severity and/or number of allergic symptoms in individuals sensitive
PT to antigens, have reduced ability to bind Immunoglobulin E.
XX
XX Disclosure; Fig 10; 100pp; English.
XX
CC The sequence represents the coding sequence of anaphylactic antigen Ara h
CC 2. Ara h 2 is an anaphylactic antigen (A), which was used to design
CC antigenic peptides having a reduced ability to bind immunoglobulin E
CC (IgE) as compared with the intact (A), or having a sequence substantially
CC identical to a portion of sequence of an antigen that includes at least
CC one IgE binding site, where at least one IgE binding site of the peptide
CC is altered. The antigenic peptides are used in a composition which is
CC useful for reducing risk or severity of allergic reaction to an antigen.
CC This is done by identifying an individual at risk of allergic reaction to
CC an antigen by identifying prior display of allergic symptoms when exposed
CC to the antigen, or a familial relationship with an individual who
CC previously displayed allergic symptoms when exposed to the antigen.
CC Following this an antigen-specific IgE present on one or more mast cells
CC or basophils in the individual's serum is identified. The individual is
CC then contacted with a peptide corresponding to a portion of the antigen,
CC which is selected, formulated, and delivered so that binding of the
CC peptide to antigen-specific IgE is reduced as compared with IgE binding
CC of intact antigen. The composition is also useful for treating and
CC preventing allergic reactions

AA
SQ Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
Query Match 66.1%; Score 474; DB 4; Length 474;
Best Local Similarity 100.0%; Pred.No. 3.8e-114;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy	2	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCTCGCTCCGACGCATCTGCGAGGCGAG	61
Db	1	CTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCTCGCTCCGACGCATCTGCGAGGCGAG	60
Qy	62	CAGTGGGAACTCCAAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGG	121
Db	61	CAGTGGGAACTCCAAAGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGG	120
Qy	122	CCCTGCGAGCAACATCTCATGCGAAGATCCAACTGTGACGAGGATTCTATGTAAACGGGAC	181
Db	121	CCCTGCGAGCAACATCTCATGCGAAGATCCAACTGTGACGAGGATTCTATGTAAACGGGAC	180
Qy	182	CCGTACAGCCCTAGTCAAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTCGA	241
Db	181	CCGTACAGCCCTAGTCAAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTCGA	240
Qy	242	TCCTCTCAGCAACCAAGAGAGGTGTGCAATCAGCTGAAACGAGTTTGAGAACAAACAAAGG	301
Db	241	TCCTCTCAGCAACCAAGAGAGGTGTGCAATGAGCTGAAACGAGTTTGAGAACAAACAAAGG	300
Qy	302	TGCATGTGCGAGGCATTGCAACAGATCATGTGAGAAACAGAGCGATAGTTGTCAGGGGAGG	361
Db	301	TGCATGTGCGAGGCATTGCAACAGATCATGTGAGAAACAGAGCGATAGTTGTCAGGGGAGG	360
Qy	362	CAACAGAGCAACAGTTTCAAGAGGGAGCTCAGGAACCTTGGCCTCAACAGTGGCGCTTAGG	421
Db	361	CAACAGAGCAACAGTTTCAAGAGGGAGCTCAGGAACCTTGGCCTCAACAGTGGCGCTTAGG	420
Qy	422	GCACACAGGGTTGCGACTTTGGACGTCGAAAGTGGCGGACAGACAGATACTAA	475
Db	421	GCACACAGGGTTGCGACTTTGGACGTCGAAAGTGGCGGACAGACAGATACTAA	474

RESULT 8
ABX70606
ID ABX70606 standard; cDNA; 474 BP.
XX
AC ABX70606;
XX
DT 26-MAR-2003 (first entry)


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XX DE Peanut Ara h2 cDNA.
XX DE
XX KW Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site;
XX KW anaphylactic food allergen; anti-allergenic; vaccine; wound healing.
XX OS Arachis hypogaea.
XX PN WO200274250-A2.
XX PD 26-SEP-2002.
XX PF 18-MAR-2002; 2002WO-US009108.
XX PR 16-MAR-2001; 2001US-0276822P.
XX PR 18-MAR-2002; 2002US-00276822.
XX PA (PANA-) PANACEA PHARM.
XX PI Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;
PI Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
PI Rabinjohn PA, Shin DS, Stanley JS;
XX WI; 2003-018765/01.
DR P-PSDB; ABUS2464.
XX PT New modified anaphylactic food allergen, useful for preventing or
XX PT treating allergic reactions associated with e.g. anaphylactic allergens.
XX PS Example 10; Fig 40; 300pp; English.
XX CC The invention relates to a modified anaphylactic food allergen has an
XX CC amino acid sequence that is substantially identical to that of natural
XX CC anaphylactic food allergen, except for a cysteine residue that has been
XX CC modified so that it cannot participate in the disulphide bond. The
XX CC modification may also comprise mutation of the IgE binding sites to
XX CC reduce allergenicity. Also included are: (1) a method of making a
XX CC modified anaphylactic food allergen; (2) a nucleotide molecule encoding
XX CC or for causing a site specific mutation in the modified anaphylactic food
XX CC allergen; (3) a transgenic plant or animal expressing the modified
XX CC anaphylactic food allergen; (4) a method of treating an individual by
XX CC reducing the clinical response to a natural anaphylactic food allergen;
XX CC and an isolated fragment of peanut allergen Ara h 1. The modified
XX CC anaphylactic food allergen is useful for preventing or treating allergic
XX CC reactions associated with any natural allergen such as food, insect,
XX CC rubber or preferably anaphylactic allergens. It is also useful for
XX CC treating wounds in mammals such as bovine, canine, feline, caprine,
XX CC ovine, porcine, murine or equine species. The present sequence is a cDNA
XX CC encoding a peanut allergen (e.g. Ara h1, h2 or h3)
SQ Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;

Query Match 66.1%; Score 474; DB 8; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.8e-114;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTGACCACTACTAGTAGCCCTGCGCTTTCTCTGCTGCCACGATCTGCGAGGAC 61
DB 1 CTGACCACTACTAGTAGCCCTGCGCTTTCTCTGCTGCCACGATCTGCGAGGAC 60

QY 62 CAGTGGGAATCCAAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTGAGG 121
DB 61 CAGTGGGAATCCAAAGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTGAGG 120

QY 122 CCCTGCGAGCAACATCTCATGCGAGAAGATCAACGTCGACGAGGATTCATATGAACGGGAC 181
DB 121 CCCTGCGAGCAACATCTCATGCGAGAAGATCAACGTCGACGAGGATTCATATGAACGGGAC 180

QY 182 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTTGA 241
DB 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTTGA 240

QY 242 TCCTCTCAGCACCAAGAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGTGAGAAACCAAGG 301

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DB 241 TCCTCTCAGCACCAAGAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAAACCAAGG 300
QY 302 TGCATGTGCCAGGCATTTGCAACAGATCATCGAGAACCGAGAGCGATAGCTTGCAGGGGAGG 361
DB 301 TGCATGTGCCAGGCATTTGCAACAGATCATCGAGAACCGAGAGCGATAGCTTGCAGGGGAGG 360
QY 362 CAACAGGAGCAACAGATTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGGCGCTTAGG 421
DB 361 CAACAGGAGCAACAGATTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGGCGCTTAGG 420
QY 422 GCACCAACAGGCTTCCGACTTGGACGCTGGAAGTGGCGGCGAGACAGATATAA 475
DB 421 GCACCAACAGGCTTCCGACTTGGACGCTGGAAGTGGCGGCGAGACAGATATAA 474

RESULT 9
ADG27517
ID ADG27517 standard; cDNA; 474 BP.
XX AC ADG27517;
XX DT 26-FEB-2004 (first entry)
XX DE Peanut cDNA encoding Ara h2.
XX KW Peanut; plant; ss; gene; allergen; Ara h1; Ara h2; Ara h3;
XX KW glycinin A2B1a; Jug n1; anti-allergic; vulnery;
XX KW anaphylactic food allergen; IgE; allergy; wound.
XX OS Arachis hypogaea.
XX PN US2003202980-A1.
XX PD 30-OCT-2003.
XX PF 18-MAR-2002; 2002US-00100303.
XX PR 29-DEC-1995; 95US-0009455P.
XX PR 23-SEP-1996; 96US-00717933.
XX PR 31-JAN-1998; 98US-0073283P.
XX PR 13-FEB-1998; 98US-0074590P.
XX PR 13-FEB-1998; 98US-0074624P.
XX PR 13-FEB-1998; 98US-0074633P.
XX PR 29-JUN-1998; 98US-00106872.
XX PR 27-AUG-1998; 98US-00141220.
XX PR 13-NOV-1998; 98US-00191593.
XX PR 29-JAN-1999; 99US-00240557.
XX PR 11-FEB-1999; 99US-00241101.
XX PR 11-FEB-1999; 99US-00248673.
XX PR 02-MAR-1999; 99US-00248674.
XX PR 02-MAR-1999; 99US-0122450P.
XX PR 02-MAR-1999; 99US-0122452P.
XX PR 02-MAR-1999; 99US-0122560P.
XX PR 02-MAR-1999; 99US-0122565P.
XX PR 11-MAR-1999; 99US-0122566P.
XX PR 28-JAN-2000; 99US-00267719.
XX PR 18-MAR-2001; 2001US-00494096.
XX PR 18-MAR-2001; 2001US-0276822P.
XX (CAPL/) CAPLAN M J.
PA (SOSI/) SOSIN H B.
PA (SAMP/) SAMPSON H.
PA (BANN/) BANNON G A.
PA (BURK/) BURKS A W.
PA (COCK/) COCKRELL G.
PA (COMP/) COMPADRE C M.
PA (CONN/) CONNAUGHTON C.
PA (HELM/) HELM R M.
PA (KING/) KING N E.
PA (KOPP/) KOPPER R A.
PA (MALE/) MALEKI S J.
PA (RABJ/) RABJOHN P A.

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(SHIN/) SHIN D. S.
 (STAN/) STANLEY J. S.
 Caplan MJ, Sosin HB, Sampson H, Bannon GA, Burks AW, Cockrell G;
 Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;
 Rabjohn PA, Shin DS, Stanley JS;
 WPI; 2003-075632/81.
 P-PSDB; ADG27518.
 New modified anaphylactic food allergen comprising a cysteine residue
 which has been modified so that it cannot participate in the disulfide
 bond, useful for treating allergic reactions or wounds.
 Example 10; SEQ ID NO 62; 194pp; English.
 The invention relates to a modified anaphylactic food allergen whose
 amino acid sequence is substantially identical to that of a natural
 anaphylactic food allergen. The natural anaphylactic food allergen
 includes at least one cysteine residue that participates in a disulphide
 bond when the natural anaphylactic food allergen is in its native
 conformation, except that the cysteine residue has been modified so that
 it cannot participate in the disulphide bond. Also included are a method
 of making a modified anaphylactic food allergen, a nucleotide molecule
 encoding a modified anaphylactic food allergen defined above, a
 nucleotide molecule for causing a site specific mutation in a gene
 encoding a natural anaphylactic food allergen, a transgenic plant or
 animal expressing a modified anaphylactic food allergen defined above, a
 method of treating an individual by reducing the clinical response to a
 natural anaphylactic food allergen by administering a modified
 anaphylactic food allergen and an isolated fragment of peanut allergen
 Ara h 1, comprising at least 10 consecutive amino acids of ADG27464 or
 ADG27465. About 10-17% of the amino acids have been modified in at least
 one IgE epitope or all the IgE epitopes recognised when the natural
 anaphylactic food allergen is contacted with serum IgE from individual(s)
 allergic to the natural anaphylactic food allergen. The invention
 discloses Peanut allergens Ara h1, Ara h2, Ara h3 (and their encoding
 cDNAs), Soybean Glycinin A2Bia and IgE-binding epitopes of the English
 walnut allergen Jug n1. The modified anaphylactic food allergen can be
 used for treating allergic reactions or wounds. The present sequence
 encodes a Peanut allergen of the invention.
 Sequence 474 BP; 132 A; 125 C; 139 G; 78 T; 0 U; 0 Other;
 Query Match 66.1%; Score 474; DB 10; Length 474;
 Best Local Similarity 100.0%; Pred. No. 3.8e-114;
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 CTCACCATCTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG 61
 1 CTCACCATCTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG 60
 62 CAGTGGGAATCTCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAGG 121
 61 CAGTGGGAATCTCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAGG 120
 122 CCCTGCGAGCAACATCTATGTCAGAAAGATCAACGCTGACGAGGATTCATATGAACGGGAC 181
 121 CCCTGCGAGCAACATCTCATGTCAGAAAGATCAACGTCGACGAGGATTCATATGAACGGGAC 180
 182 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTTGA 241
 181 CCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGAGAGGGCGCTTGA 240
 242 TCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACCAAGG 301
 241 TCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACCAAGG 300
 302 TGCATGTGCGAGGCGATTTCGAACAGATCATGAGAACCCAGAGCGATAGTTGCGAGGGGAGG 361
 301 TGCATGTGCGAGGCGATTTCGAACAGATCATGAGAACCCAGAGCGATAGTTGCGAGGGGAGG 360
 362 CAACAGGAGGCAACAGTTTCAAGAGGGGAGGCTCAGGAACTTGCCCTCAACAGTGGCGCTTAGG 421

Db 361 CAACAGGAGGCAACAGTTTCAAGAGGGGAGGCTCAGGAACTTGCCCTCAACAGTGGCGCTTAGG 420
 QY 422 GCACACACACGTTGGCAGCTTGGACGTCGAAAGTGGCGGAGAGACAGATACTAA 475
 Db 421 GCACACACACGTTGGCAGCTTGGACGTCGAAAGTGGCGGAGAGACAGATACTAA 474
 RESULT 10
 AAF90337
 ID AAF90337 standard; DNA; 682 BP.
 XX
 AC AAF90337;
 XX
 DT 11-SEP-2003 (revised)
 DT 23-JUL-2001 (first entry)
 XX
 DE Peanut allergen Ara h2 gene.
 XX
 KW Peanut; allergen; Ara h2; Ara h6; Ara h7; transgenic plant; allergy; ds.
 XX
 OS Arachis hypogaea.
 XX
 FH Key Location/Qualifiers
 CDS 59..682 /tags= a
 FT sig_peptide 59..121 /tag= b
 FT mat_peptide 122..679 /tag= c
 FT misc_feature 321..528 /tag= d
 FT /note= "PCR amplified fragment"
 XX
 PN WO200136621-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 20-NOV-2000; 2000WO-US031657.
 XX
 PR 19-NOV-1999; 99US-0167255P.
 XX
 PA (UYAL-) UNIV ALABAMA A & M.
 XX
 PI Dodo HW, Arntzen CJ, Konan KN, Viquez OM;
 XX
 DR WPI; 2001-355630/37.
 DR P-PSDB; AAB82383.
 XX
 PT Producing transgenic peanut plants that produce allergen-free seeds,
 PT useful in non-allergenic foods, by antisense or sense co-suppression of
 PT allergen-encoding genes.
 XX
 PS Claim 6; Fig 3; 72pp; English.
 XX
 CC The present sequence is that of the peanut allergen Ara h2 gene coding
 CC region. A portion of the Ara h2 gene is homologous to corresponding
 CC regions of the peanut allergen Ara h6 and Ara h7 genes. This region has
 CC been PCR amplified, cloned in transformation vectors (pUC18 and pBI434)
 CC in sense and antisense orientations and used to down-regulate the method of
 CC h6 and Ara h7 allergens in peanut. This is an example of the method of
 CC the invention, which relates to the production of a peanut plant having
 CC reduced, or undetectable, allergenic protein (AP) content in its seed. A
 CC peanut plant cell is transformed with a DNA construct containing an
 CC antisense AP gene and/or sense AP gene, or their fragments, regenerated
 CC to plants, and fertile transgenic plants that produce seeds with reduced
 CC AP content are identified. The AP sense or antisense gene may comprise at
 CC least a portion of the Ara h2 gene. The seeds are useful for preparation
 CC of allergen-free foods. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 682 BP; 170 A; 189 C; 202 G; 121 T; 0 U; 0 Other;
 Query Match 64.4%; Score 462; DB 4; Length 682;

Best Local Similarity 100.0%; Pred. No. 6.3e-111;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTCGAGGCA 60
DB 67 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTCGAGGCA 126
QY 61 GCAGTGGGAACTCAAGGAGACAGAAGATGCCAGGCCAGCTCGAGAGGGCGAACCTTGAG 120
DB 127 GCAGTGGGAACTCAAGGAGACAGAAGATGCCAGGCCAGCTCGAGAGGGCGAACCTTGAG 186
QY 121 GCCCTGGCAGCAATCTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA 180
DB 187 GCCCTGGCAGCAATCTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA 246
QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240
DB 247 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 306
QY 241 ATCTCTTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300
DB 307 ATCTCTTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 366
QY 301 GTGATGTGCGAGGATTCGAAACGATCATGAGAACCCAGAGCGATAGGTTGCGAGGGAG 360
DB 367 GTGATGTGCGAGGATTCGAAACGATCATGAGAACCCAGAGCGATAGGTTGCGAGGGAG 426
QY 361 GCAACAGGACACAGTTCAAGAGGAGCTCAGAACTTCGCTCAACAGTGCGGCCCTTAG 420
DB 427 GCAACAGGACACAGTTCAAGAGGAGCTCAGAACTTCGCTCAACAGTGCGGCCCTTAG 486
QY 421 GGCAACACAGCGTTGCGACTTTGACGCTCGAAAGTGGCGGCGAG 462
DB 487 GGCAACACAGCGTTGCGACTTTGACGCTCGAAAGTGGCGGCGAG 528

RESULT 11

AAF90336
ID AAF90336 standard; DNA; 1162 BP.
XX
AC AAF90336;
XX
DT 11-SEP-2003 (revised)
DT 23-JUL-2001 (first entry)
XX
DE Peanut allergen Ara h2 gene.
XX
XW Peanut; allergen; Ara h2; transgenic plant; allergy; ds.
XX
OS Arachis hypogaea.
XX
PH Key Location/Qualifiers
FT TATA_signal 39..46
FT /*tag= a
FT CDS 110..733
FT /*tag= b
FT sig_peptide 110..172
FT /*tag= c
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FT /*tag= d
FT polyA_signal 1060..1065
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XX
PN WO200136621-A2.
XX
PD 25-MAY-2001.
XX
XX 20-NOV-2000; 2000WO-US031657.
XX
PR 19-NOV-1999; 99US-0167255P.
XX
PA (UYAL-) UNIV ALABAMA A & M.
XX

PI Dodo HW, Arntzen CJ, Konan KN, Viquez OM;
XX WPI; 2001-355630/37.
DR P-PSDB; AAB82383.
XX
PT Producing transgenic peanut plants that produce allergen-free seeds, useful in non-allergenic foods, by antisense or sense co-suppression of allergen-encoding genes.
XX
PS Claim 5; Fig 2; 72pp; English.
XX
CC The present sequence is that of the peanut allergen Ara h2 gene. The gene was identified following screening of genomic DNA using a probe (see AAF90342) based on the known Ara h2 cDNA sequence, subcloning of positive clones into a phagemid vector, restriction enzyme digestion, ligation with vector DNA, Southern hybridisation and sequencing. The gene encodes a 207-amino acid allergenic protein (see AAB82383). The invention relates to a method for producing a peanut plant having reduced, or undetectable, allergenic protein (AP) content in its seed. A peanut plant cell is transformed with a DNA construct containing an antisense AP gene and/or sense AP gene, or their fragments, regenerated to plants, and fertile transgenic plants that produce seeds with reduced AP content are identified. The AP sense or antisense gene may comprise at least a portion of the present sequence. The seeds are useful for preparation of allergen-free foods. Recombinant AP may be produced and used to produce antibodies useful for detecting AP in foods, and for treatment or prevention of peanut allergy. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 1162 BP; 272 A; 325 C; 329 G; 236 T; 0 U; 0 Other;

Query Match 64.4%; Score 462; DB 4; Length 1162;
Best Local Similarity 100.0%; Pred. No. 7.8e-111;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTCGAGGCA 60
DB 118 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCACTCTCGAGGCA 177
QY 61 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG 120
DB 178 GCAGTGGGAACTCCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTTGAG 237
QY 121 GCCCTGGCAGCAATCTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA 180
DB 238 GCCCTGGCAGCAATCTCATGCAGAAGATCCAACTGACGAGGATTCATATGAACGGGA 297
QY 181 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 240
DB 298 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGGAGAGCGCTGG 357
QY 241 ATCTCTTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 300
DB 358 ATCTCTTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAAACGAGTTTGAGAACCAACAAAG 417
QY 301 GTGATGTGCGAGGCAATTCGAAACGATCATGGAAGAACGAGCGATAGGTTGCGAGGGAG 360
DB 418 GTGATGTGCGAGGCAATTCGAAACGATCATGGAAGAACGAGCGATAGGTTGCGAGGGAG 477
QY 361 GCAACAGGACACAGTTCAAGAGGAGCTCAGAACTTCGCTCAACAGTGCGGCCCTTAG 420
DB 478 GCAACAGGACACAGTTCAAGAGGAGCTCAGAACTTCGCTCAACAGTGCGGCCCTTAG 537
QY 421 GGCAACACAGCGTTGCGACTTTGACGCTCGAAAGTGGCGGCGAG 462
DB 538 GGCAACACAGCGTTGCGACTTTGACGCTCGAAAGTGGCGGCGAG 579

RESULT 12
AAF90342
ID AAF90342 standard; DNA; 80 BP.
XX
AC AAF90342;

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 3685.01 Seconds
(without alignments)
10880.347 Million cell updates/sec

Title: US-10-728-051-2

Perfect score: 717

Sequence: 1 gtcaccatactagtagcccc.....taaaagatcatgttttgg 717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959655780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_est7:*
- 7: gb_est8:*
- 8: gb_est9:*
- 9: gb_est10:*
- 10: gb_est11:*
- 11: gb_est12:*
- 12: gb_est13:*
- 13: gb_est14:*
- 14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686.4	95.7	788	CD038434	CD038434 UTPPI007
2	666	92.9	689	CD038213	CD038213 UTPPI004
3	555.2	77.4	732	CD038384	CD038384 UTPPI006
4	524	73.1	524	CD0897505	CD0897505 EST000010
5	487.8	68.0	634	CD038323	CD038323 UTPPI005
6	315	43.9	405	CD038306	CD038306 UTPPI005
7	289	40.3	308	CD038459	CD038459 UTPPI007
8	283.4	39.5	375	CD0897504	CD0897504 EST000009
9	223.8	31.2	696	CD038415	CD038415 UTPPI006
10	215.2	30.0	732	CD038394	CD038394 UTPPI006
11	208.8	29.1	661	CD038326	CD038326 UTPPI005
12	147.8	20.6	255	CZ550856	CZ550856 02S0166-0
13	143.4	20.0	211	CD0897508	CD0897508 EST000013
14	137.6	19.2	286	CD0897506	CD0897506 EST000011
15	133.2	18.6	680	CD038092	CD038092 UTPPI002
16	131.8	18.4	351	CD0897507	CD0897507 EST000012
17	129.6	18.1	714	CD038841	CD038841 UTPPI012
18	86	12.0	638	DT454366	DT454366 UWA065 cd
19	86	12.0	638	DT454367	DT454367 UWA066 cd

20	81	11.3	290	8	CO897509	CO897509 EST000014
21	71.6	10.0	659	8	CN825259	CN825259 LJPEST4f3
22	67.6	9.4	305	4	CD038103	CD038103 UTPPI002
23	65.8	9.2	445	7	BF594963	BF594963 su74h01.y
24	63	8.8	719	7	BE661358	BE661358 442 GmaxS
25	62.6	8.7	707	7	BE658140	BE658140 GM700005A
26	62.4	8.7	479	2	BG237204	BG237204 saa98a03.y
27	60.6	8.5	504	1	AJ498204	AJ498204 AJ498204
28	59.8	8.3	468	1	AI960869	AI960869 sc91g03.y
29	59.2	8.3	469	7	AW279501	AW279501 sf90d06.y
30	59.2	8.3	469	7	AW318110	AW318110 sg60e10.y
31	59.2	8.3	471	7	AW318155	AW318155 sg61b03.y
32	59.2	8.3	474	7	AW318193	AW318193 sg62c02.y
33	59.2	8.3	475	7	AW395515	AW395515 sg72b07.y
34	59.2	8.3	475	7	AW395679	AW395679 sg73h12.y
35	59.2	8.3	475	7	AW398039	AW398039 sg71d12.y
36	59.2	8.3	477	1	AI759696	AI759696 sb62h10.y
37	59.2	8.3	479	7	BF595027	BF595027 su74e01.y
38	59.2	8.3	479	7	AW395742	AW395742 sg74g08.y
39	59.2	8.3	481	7	AW396869	AW396869 sg64c10.y
40	59.2	8.3	482	7	AW397141	AW397141 sg67d07.y
41	59.2	8.3	486	1	AI941225	AI941225 sb66b06.y
42	59.2	8.3	487	7	AW397497	AW397497 sg79f01.y
43	59.2	8.3	489	7	BF596512	BF596512 su72c09.y
44	59.2	8.3	490	1	AI748087	AI748087 sb48a09.y
45	59.2	8.3	490	7	AW397370	AW397370 sg78a09.y

ALIGNMENTS

RESULT 1
LOCUS CD038434 788 bp mRNA linear EST 07-MAY-2003
DEFINITION UTPPI007 C04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
ACCESSION CD038434 Arachis hypogaea cDNA clone UTPPI007_C04 5', mRNA sequence.
VERSION CD038434.1 GI:30420272
KEYWORDS EST.
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 788)
AUTHORS Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
TITLE Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL Unpublished (2003)
COMMENT Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.

FEATURES
source

Location/Qualifiers
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/organism="Arachis hypogaea"
/mol_type="mRNA"
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/lab_host="XLI-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection

and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIzol-Reagent ultrapure (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 95.7%; Score 686.4; DB 4; Length 788;
Best Local Similarity 99.7%; Pred. No. 6.7e-160;
Matches 698; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
1 GCTCACCATACTAGTAGCCCTCCCTTTCTCTCGCTGCCACGCGCATCTGCGAGGCA 60
90 GCTCACCATACTAGTAGCCCTCCCTTTCTCTCGCTGCCACGCGCATCTGCGAGGCA 149
61 GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 120
150 GCAGTGGGAACCTCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 209
121 GCCTCGGAGCACATCTCATGCAGAGATCCAACTGACGAGGATTCATATGAACGGGA 180
210 GCCTCGGAGCACATCTCATGCAGAGATCCAACTGACGAGGATTCATATGAACGGGA 269
181 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGGCGCTGG 240
270 CCGGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCATATGATCGGAGGGCGCTGG 329
241 ATCCTCTCAGCACCAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 300
330 ATCCTCTCAGCACCAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAG 389
301 GTGCATGTCGAGGCATTCACACAGATCATGGAGAACGAGCGATAGTTGCGAGGGAG 360
390 GTGCATGTCGAGGCATTCACACAGATCATGGAGAACGAGCGATAGTTGCGAGGGAG 449
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510 GGCACACAGCGTTGCGACTTGCACTGCAAGTGGCGGCGAGACAGATATAACACCC 569
481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAATAGCTTATATATAGCTATTATCTATG 540
570 TATCTCAAAAAAGAAAAAGAAAAAGAAAAAGAAATAGCTTATATATAGCTATTATCTATG 629
541 GTTATGTTTGGTATTAATAAGATCATCATATATGATGATGTTGATCGTGTTA 600
630 GTTATG-TTATGTTTGGTATTAATAAGATCATCATATATGATGATGTTGATCGTGTTA 688
601 ACTAAGCGAAGCTTAGGTTATATGAGCCTTTAGAGTGCTTTATGGGCTGTCTATGT 660
689 ACTAAGCGAAGCTTAGGTTATATGAGCCTTTAGAGTGCTTTTATGGGCTGTCTATGT 748
661 TTTGTTGCTGCAGAGTTGTAAACCATCTTGAATAATATAA 700
749 TTTGTTGCTGCAGAGTTGTAAACCATCTTGAATAATATAA 788

RESULT 2
CD038213

LOCUS CD038213 689 bp mRNA linear EST 07-MAY-2003
DEFINITION UTPI004 A09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPI004_A09 5', mRNA sequence.
ACCESSION CD038213
VERSION CD038213.1 GI:30420051
KEYWORDS EST.
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschomeneae; Arachis.
1 (bases 1 to 689)
REFERENCE Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
CONTACT: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3
Location/Qualifiers
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/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13;
(NCV1XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."

Query Match 92.9%; Score 666; DB 4; Length 689;
Best Local Similarity 99.6%; Pred. No. 8e-155;
Matches 677; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 38 GCTGCCACGCGATCTCGAGGCGAGCTGGGAACCTCAAGGAGACAGAGATGCCAGAGC 97
DB 1 GCTGCCACGCGATCTCGAGGCGAGCTGGGAACCTCAAGGAGACAGAGATGCCAGAGC 60
QY 98 CAGCTCGAGAGGGCGAACCTGAGGGCCCTCGAGCAACATCTCATGAGAAGATCCAAAGCT 157
DB 61 CAGCTCGAGAGGGCGAACCTGAGGGCCCTCGAGCAACATCTCATGAGAAGATCCAAAGCT 120
QY 158 GACGAGGATTCATATGAACGGGACCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGT 217
DB 121 GACGAGGATTCATATGAACGGGACCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGT 180

ORIGIN

```
Qy 218 CCATATGATCGAGAGCGCTGGATCTCTCAGCAACCAAGAGAGGTGTGCAATGAGCTG 277
D 181 CCATATGATCGAGAGCGCTGGATCTCTCAGCAACCAAGAGAGGTGTGCAATGAGCTG 240
Qy 278 AACGAGTTTGAGAACCAACCAAGGTGATGTCGAGGAGCTTGCACAGATCATGGAGAAC 337
D 241 AACGAGTTTGAGAACCAACCAAGGTGATGTCGAGGAGCTTGCACAGATCATGGAGAAC 300
Qy 338 CAGAGCGATAGTTTGCAGGGAGGCAACAGAGCAACAGATTTCAAGAGGGAGCTCAGGAAC 397
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D 540 ATATGAATGTTGATCGTGTAACTAAGCAAGCTTAGGTTATATGATGACACCTTTTAGAG 599
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Qy 698 TAAAGATCATGTTTGT 717
D 660 TAAAGATCATGTTTGT 679
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RESULT 3
LOCUS CD038384
DEFINITION UTTP1006_E02 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
ACCESSION CD038384
VERSION CD038384.1 GI:30420222
KEYWORDS EST.
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 732)
Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.
and Lynch, R. E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.
Location/Qualifiers
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/db_xref="taxon:3818"
/clone="UTPP1006_E02"
/tissue_type="Immature pods"
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/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCv1XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adaptors. The lamda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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ORIGIN

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Query Match 77.4%; Score 555.2; DB 4; Length 732;
Best Local Similarity 93.1%; Pred. No. 3.3e-127;
Matches 617; Conservative 0; Mismatches 9; Indels 37; Gaps 2;
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Qy 61 GCAGTGGGAACCTCAAGGAGACAGAGATCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 120
D 130 GCAGTGGGAACCTCAAGGAGACAGAGATCCAGAGCCAGCTCGAGAGGGCGAACCTGAG 189
Qy 121 GCCCTCGAGCAACATCTCATGCGAAGATCCAAACGTGACGAGGATTCATATGAACGGGA 180
D 190 GCCCTCGAGCAACATCTCATGCGAAGATCCAAACGTGACGAGGATTCATATGAACGGGA 249
Qy 181 CCCGTACAGCCCTAGTCAG-----GATCC 204
D 250 CCCGTACAGCCCTAGTCAGGATCCGTACAGCCCTAGTCAGGAGCCCGACAGAGCTGATCC 309
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D 310 GTACAGCCCTAGTCATATGATCGAGAGCGCTGGATCTCTCAGACCAAGAGAGGTG 369
Qy 265 TTGCAATGAGCTGAACGAGTTTGAGAAACCAACCAAGGTGATGTGCGAGGCATTTGCAACA 324
D 370 TTGCAATGAGCTGAACGAGTTTGAGAAACCAACCAAGGTGATGTGCGAGGCATTTGCAACA 429
Qy 325 GATCATGGAGAACACAGAGCATAGTTTGCAGGGAGGCAACAGAGCAACAGTTCAAGAG 384
D 430 GATAATGGAGAACACAGAGCATAGTTTGCAGGGAGGCAACAGAGCAACAGTTCAAGAG 489
Qy 385 GGAGCTCAGGAACCTCGCTCAACAGTCGCGCTTAGGGACCAACAGAGCTTGGACTTGGGA 444
D 490 GGAGCTCAGGAACCTCGCTCAACAGTCGCGCTTAGGGACCAACAGAGCTTGGACTTGGGA 549
Qy 445 CGTCGAAAAGTGGCGGAGACAGATACATAAACACCTTATCTCAAAAAAGAAAGAAAG 504
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Qy 505 AAAAGAAAATAGCTTATATATAAGCTATTATCTATGTTTATGTTTGTGTTAATAAT 564
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D 669 AAGATCATCACTATATGAATGTTGATCGTGTAACTAAGCAAGCTTAGGTTTATG 728
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QY 625 AGC 627
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Db 729 AGC 731

RESULT 4
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DEFINITION mRNA sequence.
ACCESSION CO897505 524 bp mRNA linear EST 13-AUG-2004
VERSION CO897505.1 GI:51237295
KEYWORDS Arachis hypogaea (peanut)
SOURCE Arachis hypogaea
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 524)
Yan, Y.S., Wang, L., Zhong, Y.J., and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of peanut
Unpublished (2004)
Contact: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
Guangzhou, 510275, China
Tel: (860)02084036592
Email: yys9803@yahoo.com.cn
Seq primer: pTriplEx2 Forward.
Location/Qualifiers
1. .524
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="Yueyou 523"
/db_xref="taxon:3818"
/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone_lib="Peanut Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"

FEATURES
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1. .524
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="Yueyou 523"
/db_xref="taxon:3818"
/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone_lib="Peanut Lambda Express library"
/note="Organ: Seed; Vector: lambdaTriplEx2"

ORIGIN
Query Match 73.1%; Score 524; DB 8; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.8e-119;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AGCCCTCGCCCTTTCTCTCTGCTGCCCCACGCATCTGCGAGGAGCGAGTGGGAATCCA 75
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Db 1 AGCCCTCGCCCTTTCTCTCTGCTGCCCCACGCATCTGCGAGGAGCGAGTGGGAATCCA 60

QY 76 AGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGGCCCTGCGAGCAACA 135
|||
Db 61 AGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTCGAGGCCCTGCGAGCAACA 120

QY 136 TCTCATGCAGAAATCAACGTGACAGGATTCATATGAACGGGACCCGTACAGCCCTAG 195
|||
Db 121 TCTCATGCAGAAATCAACGTGACAGGATTCATATGAACGGGACCCGTACAGCCCTAG 180

QY 196 TCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGGATCTCTCAGCACCA 255
|||
Db 181 TCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGGATCTCTCAGCACCA 240

QY 256 AGAGAGGTGTGCAATGAGCTGAACGAGTTTGAGAACCAAGAGTGCAATGTCGAGGC 315
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Db 241 AGAGAGGTGTGCAATGAGCTGAACGAGTTTGAGAACCAAGAGTGCAATGTCGAGGC 300

QY 316 ATTGCAACAGATCATGGAGAACAGACCGATAGTTTCAGGGGAGGCAACAGGAGCAACA 375
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Db 301 ATTGCAACAGATCATGGAGAACAGACCGATAGTTTCAGGGGAGGCAACAGGAGCAACA 360

QY 376 GTTTCAGAGGAGGCTCAGGAATTCCTCAACAGTGGCGCTTAGGGCACACAGGCTTG 435
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Db 361 GTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGGCGCTTAGGGACCACAGCGTTG 420
|||
QY 436 CGACTTTGGACGTGAAAGTGGCGGCGAGACAGATATAACACCTATCTCAAAAAAGA 495
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Db 421 CGACTTTGGACGTGAAAGTGGCGGCGAGACAGATATAACACCTATCTCAAAAAAGA 480
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QY 496 AAAGAAAAAGAAAAGTAAGCTTATATATATAGCTATTATCTAT 539
|||
Db 481 AAAGAAAAAGAAAAGTAAGCTTATATATATAGCTATTATCTAT 524
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RESULT 5
CD038323
LOCUS 634 bp mRNA linear EST 07-MAY-2003
DEFINITION UTPPI005_F05 USDA-Tifton Peanut Immature Pod cDNA library (UTPP)
Arachis hypogaea cDNA clone UTPPI005_F05 5', mRNA sequence.
ACCESSION CD038323
VERSION CD038323.1 GI:30420161
KEYWORDS EST
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 634)
Luo, M., Dang, P., Guo, B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
Contact: Baozhu Guo
Molecular Genetics
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.
Location/Qualifiers
1. .634
/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"
/db_xref="taxon:3818"
/clone="UTPPI005_F05"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="XL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCV11XR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."

FEATURES
source
1. .634
/organism="Arachis hypogaea"
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/clone="UTPPI005_F05"
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/dev_stage="R6"
/lab_host="XL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site_1: EcoRI; Site_2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCV11XR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN
Query Match 68.0%; Score 487.8; DB 4; Length 634;
Best Local Similarity 91.1%; Pred. No. 2e-110;


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Db      361  ACACGGTTGGACTT 375
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LOCUS   CD038415
DEFINITION
UTPPI006_H11 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI006_H11 5', mRNA sequence.
ACCESSION
VERSION CD038415
KEYWORDS CD038415.1 GI:30420253
SOURCE  EST.
ORGANISM Arachis hypogaea (peanut)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
          Aeschynomeneae; Arachis.
REFERENCE
AUTHORS 1 (bases 1 to 696)
          Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
          and Lynch,R.E.
TITLE    Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL  Unpublished (2003)
COMMENT  Contact: Baozhu Guo
          Molecular Genetics
          USDA/ARS, Crop Protection and Management Research Unit
          2747 Davis Rd., Tifton, GA 31794, USA
          Tel: 229-387-2334
          Fax: 229-387-2321
          Email: bguo@tifton.usda.gov
          Seq primer: T3.
          Location/Qualifiers
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              /mol_type="mRNA"
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              /tissue_type="Immature pods"
              /dev_stage="R6"
              /lab_host="X11-blue"
              /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
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              /notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
              cDNA library was constructed from peanut cultivar A13
              (NCV1XAR4). A13 has resistance to Aspergillus infection
              and drought tolerance. The immature pods that developed to
              R6 stage were collected from different plants, and placed
              into liquid N2 immediately and stored in -80oC freezer.
              Total RNA was isolated with TRIzol-Reagent
              ultrapure (GIBCOBRL). mRNA was extracted and purified from
              total RNA (Promega). cDNA synthesis and library
              construction followed the protocol of By ZAP-cDNA Gigapack
              III Gold cloning kit (Stratagene). The cDNA above 500bp
              were collected after size-fraction. The inserts were
              directionally cloned into Uni-ZAP XR vector using XhoI
              EcoRI sites adapters. The lambda library was packed into
              phages using Gigapack III Gold (Stratagene). The
              un-amplified library was used to excise pBluescript
              phagemids from the Uni-ZAP XR vector, and the phagemids
              was used to transform the host bacteria SOLR. The library
              was constructed by Dr. Meng Luo and Dr. Phat Dang."

FEATURES
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  1..732
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    /cultivar="A13"
    /db_xref="taxon:3818"
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    /tissue_type="Immature pods"
    /dev_stage="R6"
    /lab_host="X11-blue"
    /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
    (UTPP)"
    /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
    cDNA library was constructed from peanut cultivar A13"

ORIGIN
Query Match 31.2%; Score 223.8; DB 4; Length 696;
Best Local Similarity 71.9%; Pred. No. 1.2e-44;
Matches 346; Conservative 0; Mismatches 107; Indels 28; Gaps 3;

Qy      219  CATATGCGAGAGCGCTGGATCTCTCAGCAACCAAGAGAGGTGTGCATGAGCTGA 278
Db      234  CCTACGATATTAGGAGTACTCGATCTCCGACCACCAACAGAGGTGCTCGGATGCTGA 293
Qy      279  ACGAGTTTGAGAACCAACCAAGGTGCATGTGCGAGGCGATTGCAACAGATCATGGAGAAC 338
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Db      294  ACCAGATGGAGAAACACACAGAGATGCATGTGCGAGGCGATTGCAGCAGATAATGGAAC 353
|||||
Qy      339  AGAGCGATAGTTGCGAGGAGGCAACAGAGCAACAGTTTCAGAGGAGGCTCAGGAAC 398
|||||
Db      354  AGTGCAGATAGTTGCGAGGAGGCAACAGTTTCAGAGGAGGCTCAGGAAC 413
|||||
Qy      399  TGCTCAACAGTGGCGCTTTAGGGCCACACAGGCTTCCGACTTGGACGTGCAAAAGTGGCG 458
|||||
Db      414  TGCCCAACAGTGAACCTTTAGGGCCACACAGGTTGCGATTGGACGT-----GA 464
|||||
Qy      459  GCAGAGACAGATACCTAAACACCTATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCT 518
|||||
Db      465  GTGGCGCAGATGCTAGACTCAAAAAATAATACTGTGCCAAAAACAACTAGTAGGAAGT 524
|||||
Qy      519  TATATATAGCTATTATCTATGCTTATGTTTATGTTTGGTAAATAATAAGATCATCACTA 578
|||||
Db      525  AGCTTATGAGCTATTATGTAATGCTT-----GTTTCGTTAAATAATAACATCATCACTG 577
|||||
Qy      579  TATGAATGCTTGCATGCTGTTAACTAAGCAAGCTTAGGTTATATATAGCACCTTTAGAGT 638
|||||
Db      578  TATGAATGCTGAT-----AGTAGTAAGTTATATAGAGCCCTTCGGTGT 625
|||||
Qy      639  GCTTTTATGCGGTTGCTCTATGTTTGTGCTGCAGAGTGTCTAACCATCTTTGAAATAATAT 698
|||||
Db      626  GCTCTTATGCTTTTACCTGTTGTTTGTCTACTGCAAAAGTTTAAACCACCATGAAATAAAG 685
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Qy      699  A 699
Db      686  A 686

```

(NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapur (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 30.0%; Score 215.2; DB 4; Length 732;
 Best Local Similarity 72.0%; Pred. No. 1.7e-42;
 Matches 347; Conservative 0; Mismatches 108; Indels 27; Gaps 4;

QY 219 CATATGATCGAGAGGCGCTTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGA 278
 DB |||||
 QY 262 CTTACGATATTAGAGTACTCGATCTCCGACCAGCAACAGAGGTGCTCGGATGAGCTGA 321
 DB |||||
 QY 279 ACAGTTTGGAAACCAAGGTGATGTGCGAGGCAATGCAACAGATCATCGAGAACC 338
 DB |||||
 QY 322 ACCAGATGGAACACACAGAGATGCATGTGCGAGGCAATGCGAGAGATAATGGAGAACC 381
 DB |||||
 QY 339 AGAGCATAGTTGCGAGGGAGGCAACAGAGCAACAGTTCAAGAGGGAGCTCAGGAAC 398
 DB |||||
 QY 382 AGTGCATAGTTGCGAGGAGGCAAAATGTCGACGAGTTCAAGAGAGAGCTCATGAAC 441
 DB |||||
 QY 399 TGCTCAACAGTGGCGCTTAGGCGCACACAGGTGTGCGACTTGGAGCTGGAAGTGGCG 458
 DB |||||
 QY 442 TGCCCAACAGTGTAACTTTAGGCGCACACAGGTGTGCGATTTGGAGCT---GAGTGGCG 498
 DB |||||
 QY 459 GCAGACAGATACCTAAACACCTATCTCAAAAAGAAAAGAAAAGAAAAGAAAATAGCT 518
 DB |||||
 QY 499 GCAGATGCTAGACTCAAAAATAATAATCTGTGCGCAAAACAACTTAGTAGGAAGTAGCT 558
 DB |||||
 QY 519 TATATAGCTAATCTATGTTATGTTTGTGTTTGTGTAATAATAAGATCATCACTA 578
 DB |||||
 QY 559 ATATTAGCTATTATGATGCTT-----GTTTCGTTAATAATAATAATATCATCACTG 611
 DB |||||
 QY 579 TATGAATGTGTTGATCGTTTAACAGGCAAGCTTAGGTTATATAGCACCTTTAGAGT 638
 DB |||||
 QY 612 TATGAATGTGCTAT-----AGTAAAGTTATATAGCACCTTCGGTGT 655
 DB |||||
 QY 639 GCTTTTATGCG-GTTGCTATGTTTGTGCTGAGAGTTGTAAACCATTTGAAATAATA 697
 DB |||||
 QY 656 GCTCTTATGCTTTACCTATGTTTGTCTACTGCAAAAGTTTAAACCATTAATAAATAA 715
 DB |||||
 QY 698 TA 699
 DB 716 GA 717

RESULT 11

CD038326
 LOCUS 661 bp mRNA linear EST 07-MAY-2003
 DEFINITION UTPI005_F10 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
 Arachis hypogaea cDNA clone UTPI005_F10 5', mRNA sequence.
 CD038326
 ACCESSION CD038326.1 GI:30420164
 VERSION
 KEYWORDS Arachis hypogaea (peanut)
 SOURCE Arachis hypogaea
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Aeschynomeneae; Arachis.
 1 (bases 1 to 661)
 Luo.M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G. and Lynch,R.E.
 Generation and Analyses of ESTs for Arachis hypogaea
 Unpublished (2003)
 Contact: Baozhu Guo
 Molecular Genetics
 USDA/ARS, Crop Protection and Management Research Unit
 2747 Davis Rd., Tifton, GA 31794, USA
 Tel: 229-387-2334
 Fax: 229-387-2321
 Email: bguo@tifton.usda.gov
 Seq primer: T3

FEATURES

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1..661
 /organism="Arachis hypogaea"
 /mol_type="mRNA"
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 /db_xref="taxon:3818"
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 /dev_stage="R6"
 /lab_host="X11-blue"
 /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
 /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80°C freezer. Total RNA was isolated with TRIzol-Reagent ultrapur (GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 29.1%; Score 208.8; DB 4; Length 661;
 Best Local Similarity 65.1%; Pred. No. 6.4e-41;
 Matches 457; Conservative 0; Mismatches 164; Indels 81; Gaps 7;

QY 4 CACATACGTAGTACCTCGCCCTTTTCTCTCGTCCCGCATCTGC---GAGGCA 60
 DB |||||
 QY 25 CACCATCTGTGTAGCCCTCTCTGCGTGTGGGACACGCTTCCGCGATGAGCG 84
 DB |||||
 QY 61 GCAGTGGGAATCCAAAGGAGAC---AGAAGATGCCAGAGCCAGCTCGAGAGGGCGAACCT 117
 DB |||||
 QY 85 CGAGAGGGGCGACAAGGGGACTCATCAAGCTCGAGAGCGAGGTAGACAGGGTGAACCT 144
 DB |||||
 QY 118 GAGGCCCTTCGAGCAACATCTCATGCAGAAAGATCCAAACGTGACGAGATTTCATATGAACG 177
 DB |||||
 QY 145 CAAGCCCTTCGAGCAGCACATAATGCAGAGGATAATGGGCGAGCAAGAGCAGTACGACT- 203
 DB |||||
 QY 178 GGACCGGTACAGCCCTTAGTCAGATCCGTACACCCCTAGTCCATATGATCGGAGGCGC 237
 DB |||||
 QY 204 -----CCTACGATATTAGGATAC 222
 DB |||||
 QY 238 TGGATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACACCA 297
 DB |||||
 QY 223 TCGATCTCCGACAGCAACAGAGGTGCTCGGATGAGTGGACCAAGTGAAGAACACAGA 282
 DB |||||
 QY 298 AAGTGCATGTGCGAGGCATTGCAACAGATCATGTGGAGAACACAGAGCGATAGTTGCAAGG 357
 DB |||||

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Db 283 GAGATGATGTCGAGGCGATTGAGCAGAGATAATGGAGAACCGAGTGGCATAGTTGTCAGGA 342
QY 358 GAGCGAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCTCAACAGTGGCGCCT 417
Db 343 CAGGCAATGGTGCAGCAGTTCAAGAGAGAGCTCATGAACCTTGCTCAACAGTGAACCT 402
QY 418 TAGGGCCACCAAGCGTTGCGACTTGGACGTCGAAAGTGGCGGCGAGAGACAGATACTAAAC 477
Db 403 CAGGGCCACCAAGCGTTGCGACTTGGACGT-----GAGTGGCGGCGAGATGCTAGAC 453
QY 478 ACCTATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 537
Db 454 TCAAAAATAATAATCTGTGCGCAAAAGAAAGAAAGTGTAGGAAGTGTCTTATGAGCTATTATGT 513
QY 538 ATGGTTATGTTTGTAGTTTGTGTAATAATAAAGATCATCACTATATGAATGTGTTGATCGTG 597
Db 514 ATGCTT-----GTTTCGTTAATAATAATATATCATCTGTATGAATGTGGTGTAT----- 562
QY 598 TTAACTAAGGCAAGCTTAGCTTATATGAGCACCTTTTATGAGTGTCTTTATGCGCGTTGCTTA 657
Db 563 -----AGGTAAGGTTATATGAGCA-CTTCGGTGTCTCTTATGGCTTTACCTA 609
QY 658 TGTGTTTGTCTGCGAGAGTGTAAACCATCTTGAATAATATA 699
Db 610 TGTGTTGCTACTGCAAGTTTANCCACCNTGAATAAAAGA 651

RESULT 12
LOCUS CZ550656/c
DEFINITION 02S0166-05A1-H01 UniformMu MutAIL Library Zea mays genomic clone
ACCESSION CZ550656
VERSION 1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 255)
AUTHORS Lathaw,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.
TITLE Sequence tagged transposon insertions from the UniformMu maize population
JOURNAL Unpublished (2003)
COMMENT Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu
Sequence flanking probable Mu insertion site in UniformMu line:
02S0166-0
Class: transposon insertion site.
FEATURES
source
1..255
Location/Qualifiers
/organism="Zea mays"
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/clone="02S0166-05A1-H01"
/clone_lib="UniformMu MutAIL Library"
/notes="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

Query Match 20.6%; Score 147.8; DB 13; Length 255;
Best Local Similarity 83.9%; Pred. No. 1.1e-24;
Matches 162; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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Matches 185; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY 418 TAGGGCCACCAAGCGTTGCGACTTGGACGTCGAAAG-TGGCGGCGAGAGACAGATACTAAA 476
Db 255 TAGGGCCACCAAGCGTTGCGACTTGGACGTCGAAAGTTGGCGGCGAGAGACAGATACTTAA 196
QY 477 CACC-TATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 535
Db 195 CACCTTATCTCCAAAAAGTAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 136
QY 536 CTATGTTATGTTTGTAGTTTGTGTAATAATAAAGATCATCACTATATGAATGTGTTGATCG 595
Db 135 CTATGTTATG-TTAGTTTGTGTAATAATAAAGATCATCACTATATGAATGTGTTGATCG 77
QY 596 TGTTAACTAAGGCAA 610
Db 76 TGTTAAACATAGACAA 62

RESULT 13
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DEFINITION CO897508 Peanut Lambda Express library Arachis hypogaea cDNA 5',
mRNA sequence.
ACCESSION CO897508.1 GI:51237298
VERSION CO897508
KEYWORDS EST.
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 211)
AUTHORS Yan,Y.S., Wang,L., Zhong,Y.J. and Huang,S.Z.
TITLE Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL Unpublished (2004)
COMMENT Contact: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
Guangzhou, 510275, China
Tel: (860)02084036592
Email: yys9803@yahoo.com.cn
Seq primer: pTriplex2 Forward.
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/mol_type="mRNA"
/cultivar="Yueyou 523"
/db_xref="taxon:3818"
/tissue_type="Cotyledons"
/dev_stage="Mid-matured stage"
/lab_host="E.coli BM25.8"
/clone_lib="Peanut Lambda Express library"
/notes="Organ: Seed; Vector: lambdaTriplex2"

ORIGIN
Query Match 20.0%; Score 143.4; DB 8; Length 211;
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QY 267 GCATGAGCTGACGAGTTTGAGAACAAACCAAGGTGCATGTGCGAGGCAATTCACAGAGA 326
Db 11 GCATGAGCTGAACGAGATGGAGAACACAGAGATGCATGTGCGAGGCAATTCACAGAGA 70
QY 327 TCATGAGAACACAGACCGATAGTTTCAGGGGAGGCAACAGGAGCAACAGTTCAAGAGGG 386
Db 71 TATGAGAACACAGTCGATAGTTTCAGGACAGGCAATGTGTGACAGAGTTCAAGAGAG 130
QY 387 AGCTCAGGAACCTTGCTCAACAGTGGCGCTTAGGGCACACAGCGTTGCGACTTGGACG 446
Db 131 AGCTCATGAACCTGCCCAACAGTGTAACTTTAGGGCACACAGCGTTGCGACTTGGACG 190
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QY      447 TCGAAAGTGGCGG 459
Db      191 TGAGTGGCGGCG 203

RESULT 14
CO897506
LOCUS   EST000011 Peanut Lambda Express library Arachis hypogaea cDNA 5',
DEFINITION mRNA sequence.
ACCESSION CO897506
VERSION   CO897506.1 GI:51237296
KEYWORDS EST.
SOURCE    Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
          Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 286)
AUTHORS  Yan,Y.S., Wang,L., Zhong,Y.J. and Huang,S.Z.
TITLE    Expressed sequence tags of mid-matured cotyledons of peanut
JOURNAL  Unpublished (2004)
COMMENT  Contact: Shangzhi Huang
          Plant Development and Molecular Biology
          Sun Yat-sen University, Department of Biology and Biotechnology
          Guangzhou, 510275, China
          Tel: (860)02084036592
          Email: yys9803@yahoo.com.cn
          Seq primer: pTriplex2 Forward.
FEATURES             Location/Qualifiers
     source
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         /organism="Arachis hypogaea"
         /mol_type="mRNA"
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         /lab_host="E.coli BM25.8"
         /clone_lib="Peanut Lambda Express library"
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Best Local Similarity 80.5%; Pred. No. 3.1e-23;
Matches 161; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY      219 CATATGATCGAGAGGCGGTGGATCCTCTCAGCACCAAGAGAGGTGTTCGAATGAGCTGA 278
Db      87 CCTACGATATTGGAGTACTCGATGCTCTCCAGCACCAAGAGAGGTGTTCGATGAGCTGA 146

QY      279 ACCAGTTTGAGAACCAACCAAGGTGCGATGTGCGAGGCATTGGCAACAGATCATGGAGAAC 338
Db      147 ACAGATGGAGAACACACACAGATGATGTGCGAGGCATTGGCAGCAGATATGGAGAAC 206

QY      339 AGAGCGATAGTTTCAGGGGAGGCAACAGAGCAACAGTTTCAAGAGGAGCTCAGGAAT 398
Db      207 AGTGGATAGTTTGACGAGCAGGCAATGTGTGACGAGTTCAGAGAGAGCTCATGAAT 266

QY      399 TGCTCAACAGTGGGCTT 418
Db      267 TGCCCCAACAGTGTAACTTT 286

RESULT 15
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LOCUS   CD038092
DEFINITION UTPPI002_D04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
          Arachis hypogaea cDNA clone UTPPI002_D04 5', mRNA sequence.
ACCESSION CD038092
VERSION   CD038092.1 GI:30419930
KEYWORDS EST.

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SOURCE      Arachis hypogaea (peanut)
ORGANISM    Arachis hypogaea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
            Aeschynomeneae; Arachis.
REFERENCE   1 (bases 1 to 680)
AUTHORS     Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
            and Lynch,R.E.
TITLE       Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL     Unpublished (2003)
COMMENT     Contact: Baozhu Guo
            Molecular Genetics
            USDA/ARS, Crop Protection and Management Research Unit
            2747 Davis Rd., Tifton, GA 31794, USA
            Tel: 229-387-2334
            Fax: 229-387-2321
            Email: bguo@tifton.usda.gov
            Seq primer: T3
FEATURES     Location/Qualifiers
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         /clone="UTPPI002_D04"
         /tissue_type="Immature pods"
         /dev_stage="R6"
         /lab_host="XLI-blue"
         /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
         /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
            cDNA library was constructed from peanut cultivar A13
            (NCVILX44). A13 has resistance to Aspergillus infection
            and drought tolerance. The immature pods that developed to
            R6 stage were collected from different plants, and placed
            into liquid N2 immediately and stored in -80oC freezer.
            Total RNA was isolated with TRIzol-Reagent
            ultrapure (GIBCOBRL). mRNA was extracted and purified from
            total RNA (Promega). cDNA synthesis and library
            construction followed the protocol of by ZAP-cDNA Gigapack
            III Gold cloning kit (Stratagene). The cDNA above 500bp
            were collected after size-fraction. The inserts were
            directionally cloned into Uni-ZAP XR vector using XhoI
            EcoRI sites adapters. The lambda library was packed into
            phages using Gigapack III Gold (Stratagene). The
            un-amplified library was used to excise pBluescript
            phagemids from the Uni-ZAP XR vector, and the phagemids
            was used to transform the host bacteria SOLR. The library
            was constructed by Dr. Meng Luo and Dr. Phat Dang."
ORIGIN

Query Match      18.6%; Score 133.2; DB 4; Length 680;
Best Local Similarity 58.3%; Pred. No. 4.4e-22;
Matches 344; Conservative 0; Mismatches 213; Indels 33; Gaps 5;

QY      76 AGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACCTCAGGCCCTCGCAGCAACA 135
Db      107 AGGGGATGACCACTGTCAGAGGCGAGTTGCAAGGGGCAAACTCAGGCCCTGTGAGGAACA 166

QY      136 TCTCATGCAAGATCCACGTCACGAGGATTCATATGAACGGGACCCGTACAGCCCTAG 195
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QY      196 TCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGGGCGCTGGATCTCTCAGCACCA 255
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QY      256 AGAGAGGTGTTCGAATGAGCTGAACGAGTTTGAGAACCAACAAAGGTGCATGTCCGAGGC 315
Db      275 GCAAAGGTGCTGCAACGAGCTCAACCGGTTCCAGATATCAACAAAGGTGCATGTGCCAGGC 334

QY      316 ATTGCAACAGATCATGTGGAGAACCAAGACGCGATAGTT---GCAGGGGAGCAACAGGAGCA 372

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Result No.	Query %			DB		ID		Description
	Score	Match	Length					
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2	717	100.0	717	3	US-09-191-593-6	Sequence 6, Appl		
3	717	100.0	717	3	US-09-191-593-9	Sequence 9, Appl		
4	713.8	99.6	743	3	US-09-106-872A-1	Sequence 1, Appl		
5	462	64.4	682	3	US-09-715-036-3	Sequence 3, Appl		
6	462	64.4	1162	3	US-09-715-036-1	Sequence 1, Appl		
7	80	11.2	80	3	US-09-715-036-7	Sequence 7, Appl		
8	65.6	9.1	777	2	US-08-618-911-3	Sequence 3, Appl		
9	64	8.9	777	2	US-08-618-911-5	Sequence 5, Appl		
10	63.4	8.8	770	3	US-08-618-911-5	Sequence 1, Appl		
11	63.4	8.8	770	3	US-08-531-727-1	Sequence 1, Appl		
12	62	8.6	62	3	US-09-715-036-8	Sequence 8, Appl		
13	58.8	8.2	7218	2	US-08-232-463-14	Sequence 14, Appl		
14	54.4	7.6	723	2	US-08-618-911-1	Sequence 1, Appl		
15	48.4	6.8	25590	3	US-09-949-002-777	Sequence 777, App		
16	44.4	6.2	168104	3	US-09-949-016-12026	Sequence 12026, A		
17	44.4	6.2	168105	3	US-09-949-016-16554	Sequence 16554, A		
18	44.4	6.2	1664976	3	US-08-916-421B-1	Sequence 1, Appl		
19	44.4	6.2	1664976	3	US-09-692-570-1	Sequence 1, Appl		
20	44.2	6.2	56665	3	US-09-949-016-14026	Sequence 14026, A		
21	44	6.1	37379	3	US-09-949-016-16226	Sequence 16226, A		
22	43.6	6.1	601	3	US-09-949-016-4480	Sequence 4480, A		
23	43.6	6.1	34855	3	US-09-949-016-13004	Sequence 13004, A		

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Db			
361	GCAACAGAGCAACAGTTCAAGAGGGAGCTCAGGAA	CTTGCTTCAACAGTGCAGGCTTTAG	420
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RESULT 2

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; US-09-191-593-6
; Sequence 6, Application US/09191593
; Patent No. 6835824
; GENERAL INFORMATION:
; APPLICANT: BURKS, A Wesley, HELM, Ricki M,
; APPLICANT: COCKRELL, Gael, STANLEY, J Steven,
; APPLICANT: BANNON, Gary A
; TITLE OF INVENTION: PEANUT ALLERGENS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Head, Johnson & Kachigian
; STREET: 112 W. Center St., Suite 230
; CITY: Fayetteville
; STATE: Arkansas AR
; COUNTRY: United States of America
; ZIP: 72701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS 6.2
; SOFTWARE: Wordperfect 6.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,593
; FILING DATE: 13 NOVEMBER 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/717,933
; FILING DATE: 23 SEPTEMBER 1996
; APPLICATION NUMBER: US 07/998,377
; FILING DATE: 30 DECEMBER 1992
; APPLICATION NUMBER: US 08/158,704
; FILING DATE: 29 NOVEMBER 1993
; APPLICATION NUMBER: US 60/009,455
; FILING DATE: 29 DECEMBER 1995
; APPLICATION NUMBER: US 08/610,424
; FILING DATE: 04 MARCH 1996
; ATTORNEY/AGENT INFORMATION:
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; UNITS: No. 6835824 applicable
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..475
; IDENTIFICATION METHOD: By agreement with
; IDENTIFICATION METHOD: protein information and established
; IDENTIFICATION METHOD: consensus sequence
; OTHER INFORMATION: Seed storage protein and
; OTHER INFORMATION: allergen
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-09-191-593-6
Query Match          100.0%; Score 717; DB 3; Length 717;
Best Local Similarity 100.0%; Pred. No. 1.le-185;
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RESULT 3

US-09-191-593-9
Sequence 9, Application US/09191593
Patent No. 6835824
GENERAL INFORMATION:
APPLICANT: BURKS, A Wesley, HELM, Ricki M,
APPLICANT: COCKRELL, Gael, STANLEY, J Steven,
APPLICANT: BANNON, Gary A
TITLE OF INVENTION: PEANUT ALLERGENS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Head, Johnson & Kachigian
STREET: 112 W. Center St., Suite 230
CITY: Fayetteville
STATE: Arkansas AR
COUNTRY: United States of America
ZIP: 72701
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS 6.2
SOFTWARE: Wordperfect 6.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,593
FILING DATE: 13 NOVEMBER 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/717,933
FILING DATE: 23 SEPTEMBER 1996
APPLICATION NUMBER: US 07/998,377
FILING DATE: 30 DECEMBER 1992
APPLICATION NUMBER: US 08/158,704
FILING DATE: 29 NOVEMBER 1993

APPLICATION NUMBER: US 60/009,455
FILING DATE: 29 DECEMBER 1995
APPLICATION NUMBER: US 08/610,424
FILING DATE: 04 MARCH 1996
ATTORNEY/AGENT INFORMATION:
NAME: ALEXANDER, DANIEL R
REGISTRATION NUMBER: 32,604
REFERENCE/DOCKET NUMBER: ARK00895601B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (501) 582-9111
TELEFAX: (501) 521-4931
TELEX: No. 6835824 applicable
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 717 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: identified as Ara h II cDNA clone
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: No. 6835824 applicable
ORIGINAL SOURCE: Arachis hypogaea
ORGANISM: Arachis hypogaea
STRAIN: Florunner
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: seed
HAPLOTYPE: No. 6835824 applicable
TISSUE TYPE: seed cDNA
CELL TYPE: No. 6835824 applicable
CELL LINE: No. 6835824 applicable
ORGANELLE: No. 6835824 applicable
IMMEDIATE SOURCE:
LIBRARY: florunner seed cDNA expression
LIBRARY: library in Uni-ZAP XR vector
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT: No. 6835824 applicable
MAP POSITION: No. 6835824 applicable
UNITS: No. 6835824 applicable
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD: By agreement with
IDENTIFICATION METHOD: protein information and established
IDENTIFICATION METHOD: consensus sequence
OTHER INFORMATION: Seed storage protein and
OTHER INFORMATION: allergen
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-191-593-9

Query Match 100.0%; Score 717; DB 3; Length 717;
Best Local Similarity 100.0%; Pred No. 1,1e-185;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATAGTAGCCCTCGCCCTTTCTCTCTCGTGGCCACCGCATCTCGGAGGCA 60
Db 1 GCTCACCATAGTAGCCCTCGCCCTTTCTCTCTCGTGGCCACCGCATCTCGGAGGCA 60
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Db 61 GCAGTGGGAACCTCCAGGAGACAGAGAATGCCAGAGCCAGCTCGAGAGGGCGAACTCTGAG 120
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Db 121 GCCTCGAGCAACATCTCATGACAGAGATCCAACTGACGAGGATTCATATGAACGGGA 180
Qy 181 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
Db 181 CCGGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
Qy 241 ATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAAACGAGTGTGAGAACAAACAAAG 300
Db 241 ATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAAACGAGTGTGAGAACAAACAAAG 300
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Db 361 GCACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACCTTGCCTCAACAGTCGGGCCCTTAG 420
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RESULT 4
US-09-106-872A-1
; Sequence 1, Application US/09106872A
; Patent No. 6486311

GENERAL INFORMATION:
; APPLICANT: Burks Jr., A. Wesley
; APPLICANT: Stanley, J. Steven
; APPLICANT: Cockrell, Gael
; APPLICANT: King, Nina E.
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Helm, Ricki M.
; APPLICANT: Bannan, Gary A.
; TITLE OF INVENTION: Peanut Allergens and Methods
; FILE REFERENCE: HS 103 CIP
; CURRENT APPLICATION NUMBER: US/09/106,872A
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: PCT/US96/15222
; PRIOR FILING DATE: 1996-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 743
; ORGANISM: Arachis hypogaea

Query Match 99.6%; Score 713.8; DB 3; Length 743;
Best Local Similarity 99.7%; Pred. No. 8.3e-185;
Matches 715; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCCATCTCGGAGGCA 60
Db 6 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCACGCCATCTCGGAGGCA 65
Qy 61 GCAGTGGGAACCTCCAGGAGACAGAGAATGCCAGAGCCAGCTCGAGAGGGCGAACTCTGAG 120
Db 66 GCAGTGGGAACCTCCAGGAGACAGAGAATGCCAGAGCCAGCTCGAGAGGGCGAACTCTGAG 125
Qy 121 GCCCTGCGAGCAACATCTCATGACAGAGATCCAACTGACGAGGATTCATATGAACGGGA 180
Db 126 GCCCTGCGAGCAACATCTCATGACAGAGATCCAACTGACGAGGATTCATATGAACGGGA 185
Qy 181 CCCGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 240
Db 186 CCCGTACAGCCCTAGTCAGATCCGTACAGCCCTAGTCATATGATCGGAGGCGCTGG 245
Qy 241 ATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAAACGAGTGTGAGAACAAACAAAG 300
Db 246 ATCTCTCAGCACCAAGAGAGGTGTGCAATGAGCTGAAACGAGTGTGAGAACAAACAAAG 305
Qy 301 GTGCATGTGCGAGGCATTGCAACAGATCATGAGAACCCAGAGCGATAGGTTGCGAGGGAG 360
Db 306 GTGCATGTGCGAGGCATTGCAACAGATCATGAGAACCCAGAGCGATAGGTTGCGAGGGAG 365
Qy 361 GCACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACCTTGCCTCAACAGTCGGGCCCTTAG 420
Db 366 GCACAGGAGCAACAGTTCAGAGGGAGCTCAGGAACCTTGCCTCAACAGTCGGGCCCTTAG 425
Qy 421 GGCAACACAGCGTTGCGACTTGCAGCTCGAAAGTGGCGGAGAGAGAGATCTTAAACACC 480
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Db 546 GTTATGTTAGTTTTGGTAAATAAAGATCATCATATATGAAGTGTGATCGTGTTA 605
Qy 601 ACTAAGCGAAGCTTAGGTTATATGACACCTTTAGAGTGCTTTATGCGGTTGCTCTATGT 660
Db 606 ACTAAGCGAAGCTTAGGTTATATGACACCTTTAGAGTGCTTTATGCGGTTGCTCTATGT 665
Qy 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 717
Db 666 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 722

RESULT 5
US-09-715-036-3
; Sequence 3, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIOUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/09/715,036
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-09-715-036-3

Query Match 64.4%; Score 462; DB 3; Length 682;
Best Local Similarity 100.0%; Pred. No. 4.2e-116;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTGGAGGCA 60
DB 67 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTGGAGGCA 126
QY 61 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTGAG 120
DB 127 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTGAG 186
QY 121 GCCTGCGGAAACATCTCATGAGAAAGATCCAAAGTGAAGAGATTCATATGAACGGGA 180
DB 187 GCCTGCGGAAACATCTCATGAGAAAGATCCAAAGTGAAGAGATTCATATGAACGGGA 246
QY 181 CCCTGACAGCCCTAGTACAGTCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 240
DB 247 CCCTGACAGCCCTAGTACAGTCCGTACAGCCCTAGTCCATATGATCGGAGGCGCTGG 306
QY 241 ATCTCTCAGCACCACGAGAGGCTTGCATAGCTGAAACGAGTTTGAGAAACCAACAAAG 300
DB 307 ATCTCTCAGCACCACGAGAGGCTTGCATAGCTGAAACGAGTTTGAGAAACCAACAAAG 366
QY 301 GTGCATGTGCGAGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCAGGGGAG 360
DB 367 GTGCATGTGCGAGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCAGGGGAG 426
QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG 420
DB 427 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG 486
QY 421 GGCAACACAGCGTTGGCAGCTTGAGCGTCGAAAGTGGCGGCGAG 462
DB 487 GGCAACACAGCGTTGGCAGCTTGAGCGTCGAAAGTGGCGGCGAG 528

RESULT 6
US-09-715-036-1
; Sequence 1, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1162
; TYPE: DNA
; ORGANISM: Arachis hypogaea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (110)..(730)
US-09-715-036-1

Query Match 64.4%; Score 462; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 5.3e-116;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTGGAGGCA 60
DB 118 GCTCACCATACTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTGGAGGCA 177
QY 61 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTGAG 120

DB 178 GCAGTGGGAACTCCAAAGGAGACAGAAGATGCGAGAGCCAGCTCGAGAGGGCGAACTGAG 237
QY 121 GCCTGCGGAGCAACATCTCATGAGAAAGATCCAAAGTGAAGAGATTCATATGAACGGGA 180
DB 238 GCCTGCGGAGCAACATCTCATGAGAAAGATCCAAAGTGAAGAGATTCATATGAACGGGA 297
QY 181 CCCTGACAGCCCTAGTACAGTCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 240
DB 298 CCCTGACAGCCCTAGTACAGTCCGTACAGCCCTAGTCCATATGATCGGAGAGGCGCTGG 357
QY 241 ATCTCTCAGCACCACGAGAGGCTTGCATAGCTGAAACGAGTTTGAGAAACCAACAAAG 300
DB 358 ATCTCTCAGCACCACGAGAGGCTTGCATAGCTGAAACGAGTTTGAGAAACCAACAAAG 417
QY 301 GTGCATGTGCGAGGCAATGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCAGGGGAG 360
DB 418 GTGCATGTGCGAGGCAATGCAACAGATCATGGAGAACCCAGAGCGATAGTTGCAGGGGAG 477
QY 361 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG 420
DB 478 GCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCCTCAACAGTGGCGCTTAG 537
QY 421 GGCAACACAGCGTTGGCAGCTTGAGCGTCGAAAGTGGCGGCGAG 462
DB 538 GGCAACACAGCGTTGGCAGCTTGAGCGTCGAAAGTGGCGGCGAG 579

RESULT 7
US-09-715-036-7
; Sequence 7, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; TITLE OF INVENTION: TRANSGENIC PEANUT SEEDS
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-715-036-7

Query Match 11.2%; Score 80; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTCGGAGGAGCAGTGGGAA 70
DB 1 CTAGTAGCCCTCGCCCTTTCTCTCGCTGCCACCGCATCTCGGAGGAGCAGTGGGAA 60
QY 71 CTCCAAGGAGACAGAAGATG 90
DB 61 CTCCAAGGAGACAGAAGATG 80

RESULT 8
US-08-618-911-3
; Sequence 3, Application US/08618911
; Patent No. 5850016
; GENERAL INFORMATION:
; APPLICANT: Jung, Rudolf

QY	67	GGNACTCCAAGGAGACAGAGATGCCAGAGCCAGCTCGAGAGGGCGAACTGTAGGCCCTG	126
Db	99	GCAGCACCCAGCAAGA--TAGTGTCCGAACGCTTAAGGGGGTGAACCTTCACGCCCTG	155
QY	127	CGAGCAACATCTCATGCGAAGATCCAACTGTGCGAGGATTTCATATGAACGGGACCCGTA	186
Db	156	CGAAGACACATCATGGAGAGATCCAAGGCCGCGCGATGACGATCATGATGATGACCA	215
QY	187	CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATGATCGAGAGG-----	234
Db	216	CGACAATCACATCTTCAGAGCATTGCGGGGAAGAATCAACTACATAGCTAAGAAGGAAG	275
QY	235	-----CGTGTGATCTCTTCAGCACTAAGAGAGAGTGTTCGAATCAGCTGAACGA	282
Db	276	AAAGACGAAGACGAAGAAGGAGGACAGATGCAGAGTGTCTGCACAGAAATGAGCGA	335
QY	283	GTTTGAGAACACCAAGGTGCATGTGGAGGCAATTGCACAGATCATTGAGAACCCAGAG	342
Db	336	GCTTAAGAGCCCCNAA---TCCAGTGCMAAGCGCTGCAGAAGATAATGGAGAACCCAGAG	392
QY	343	CGATAGGTTGCAAGGGAGGCAACAGGAGCAACAGTTTCAAGAGGGAGCTCAGGAACTTGCC	402
Db	393	CGAGGAACCTGGAGGAGAGGAGAACAGAAA--ATGGAGAGGAGCTTATGAACCTTGC	449
QY	403	TCAACAGTGGCGCCTTAGGGCAACACAGCTTGGAGCTTGGACGTGGAAGTGGCGGAG	462
Db	450	TACTATGTTCAGGTTTGGGGCCCATGATCGGATGCGACTTGTCTCTCCGA-----TGACTA	503
QY	463	AGACAGATACTAAACACCTATCTCAAAAAAAGAAAAGAAAAGAAATAGCTTATA	522
Db	504	AGNAGTTAAAGCAATGTTGTCACTTGTACGTACTAACATGATGTGATGTTATGCT	563
QY	523	TATAAGCTATTATCTATGGTTATGTTTAGTTTTGGTAATATAAAGATCATCACTATATG	582
Db	564	AGCTAGCTATAACATAAAGCTGTCTCTGAGTGTGTTGTATATTAATAAGATCATCACTGG	623
QY	583	AATGTGTTGATCGCTTAACTAAGCAAGCTTAGTGTTATATGAGCACTTTACAGAGTGCTT	642
Db	624	TGAATGGTGATCGTGACGTACCTACTTACTAGTAGGCAATGGAAGCACCTTAGATGTGCTT	683
QY	643	T---TATGGCGTGTCTATGTTTTTGTGTCGACAGTTGTAACCATCTTGAAT	693
Db	684	TCGTGATGGCCTTGCTCTGTTTTGAGACTTTTGTAAATGTTTTCGAGTTTAAAT	737

Qy	403	TCAACAGTGGCGCTTTAGGGCACACAGCGTTTGGACTTGGACGTGCA - AAGTGGCGGCA	461
Db	439	TACTATGTCAGAGTTTGGACCCATGATCCAGTGGCGACTTGTCTCCGATGACTAAGAAGT	498
Qy	462	GACACAGATACATAACACACCTTATCTCAAAAAAGAAAGAAAGAAAAATAGCTTAT	521
Db	499	TAAAGCAATGTTGTCACTTGTCTACTAACAATGATGTGATAGTTTATGCTAGCT - - -	555
Qy	522	ATATAAGCTATTATCATGGTTATGTTTAGTTTGGTAAATAATAAAGATCATCACTATAT	581
Db	556	-----AGCTATAACATAAAGCTGTCTCTGAGTGTGTGTATATTAAATAAAGATCATCACTG	610
Qy	582	GAATGTGTTGATCGTGTTAACTAAGGCAAGCTTTAGGTTATATGAGCAACCTTTAGAGTGCT	641
Db	611	GTGAATGGTGATCGTGTACGTACCTTACTTAGTAGGCAATGGAAAGCACTTAGAGTGTGCT	670
Qy	642	TT-- -TATGCGTGTGCTATGTTTTGTTGCTCGAGAGTTGTAACCACTCTTGAAT	693
Db	671	TTGTGCATGCGCTTGCTCTGTTTTCGAGACTTTGTAACTGTTTTCGAGTTTAAAT	725

;	REGISTRATION NUMBER:	36,627	
;	REFERENCE/DOCKET NUMBER:	B98-003	
;	TELECOMMUNICATION INFORMATION:		
;	TELEPHONE:	(650) 343-4341	
;	TELEFAX:	(650) 343-4342	
;	INFORMATION FOR SEQ ID NO:	1:	
;	SEQUENCE CHARACTERISTICS:		
;	LENGTH:	770 base pairs	
;	TYPE:	nucleic acid	
;	STRANDEDNESS:	double	
;	TOPOLOGY:	linear	
;	MOLECULE TYPE:	cdna	
;	US-08-938-675A-1		

Query Match	8.8%;	Score 63.4;	DB 3;	Length 770;
Best Local Similarity	51.6%;	Pred. No. 2.7e-07;		
Matches 369;	Conservative 0;	Mismatches 301;	Indels 45;	Gaps

Qy	7	CATACTAGTAGCCCTCGCCCTTTTCTCTCTCGTGGCCACGCATCTCGGAGGCGAGCAGTG	66
Db	28	CACAATCCTCTCATCTCTTCTTCTGATCGCCACACTTTCGACGCGCTCCAAATG	87
Qy	67	GGAACCTCAAGGAGACAGAGATGCCAGACCCAGCTCGAGAGGCGCAACCTGAGGCCCTG	126
Db	88	GCAGCACCAAGA---TAGCTGCCCAAGCAGCTCCAGGGGTGAACCTTCAGCCCTG	144
Qy	127	CGAGCAACATCTCATGCAGAAAGATCCAACTGACAGGATTCATATGAAACGGGACCCGTA	186
Db	145	CGAGAGCACATCATGGAGAAGATCCAAAGCCCGCGCGATGACCATGATGATGACGA	204
Qy	187	CAGC-----CCTAGTCAGGATCCGTAACAGCCCTAGTCCATATGATCGGAG-----	231
Db	205	CGACAATCACTTCTCAGGACCATTGCGGGGAAGAATCAACTACATAAGGAGGAACGAAGG	264
Qy	232	-----AGGCGCTGGATCCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGA	282
Db	265	AAAAGACGAAGACGAAGAAGAAGACACATGCAGAAAGTGTGCACAGAAATGAGCGCA	324
Qy	283	GTTTGGAACAACCAAAAGGTGCATGTGCGAGGCATTGCAACAGATCATGAGAACCCAGAG	342
Db	325	GCT---GAGNAAGCCCAATGCCAGTGCAAGCGCTGCAGAGATAATGGAGAACCCAGAG	381
Qy	343	CGATAGTTGCAGGGGAGGCAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACATTGCC	402
Db	382	CGAGGAACCTGGAGGAAGCAGAAGAAGAAA---ATGGAAGAGGAGCTCATTTAACTTTGGC	438
Qy	403	TCAACAGTGGCGCTTAGGGCACCAAGCGTTGGCACTTGGACGTGCA--AAGTGGCGCGCA	461
Db	439	TACTATGTGCAGGTTTGGACCCATGATCCAGTCGCACTTGTCTCTCCGATGACTAAGAAGT	498
Qy	462	GAGACAGATACTAAACACCTATCTCAAAAAAGAAAGAAAGAAAGAAATAGCTTAT	521
Db	499	TAAAGCAATGTTGTCATTGTCGTACTAACATGATGTGATAGTTTATGCTAGCT---	555
Qy	522	ATATAAGCTATTATCTATGTTATGTTTGGTAAATAATAAAGATCATCATATAT	581
Db	556	-----AGCTATAACATAAGCTGCTCTCTGAGTGGTTGCTATATTAAATAAAGATCATCACTG	610
Qy	582	GAATGTGTTGATCGTTAACTAAGGCAAGCTTAGGTTATATGAGCACTTTTAGAGTGTCT	641
Db	611	GTGAATGGTGATCGTGTACGTACCCCTACTTTAGTAGGCAATGGAAGCACTTAGAGTGTGCT	670
Qy	642	TT---TATGCGTTGCTATGTTTGTGCTGCAGAGTGTGTAACCATCTTTGAAAT	693
Db	671	TTGTGATGCCCTTGCTCTGTTTGAGACCTTTTGAATGTTTTCGAGTTTAAAT	725

RESULT 11	
US-09-531-727-1	
; Sequence 1, Application US/09531727	
; Patent No. 6544956	
; GENERAL INFORMATION:	
; APPLICANT: de Lumen, Benito O.	

RESULT 11
US-09-531-727-1
; Sequence 11, Application US/09531727
; Patent No. 654956
; GENERAL INFORMATION:
; APPLICANT: de Lumen, Benito O.


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; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 25590
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(25590)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-777

Query Match      6.8%; Score 48.4; DB 3; Length 25590;
Best Local Similarity 50.9%; Pred. No. 0.016;
Matches 115; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 488 AAAAAGAAAGAAAGAAAGAAAGAAATAGCTTATATATAGCTATTATCTATGTTATGT 547
Db 4123 AATAGATATTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATA 4064

Qy 548 TTAGTTTGGTAAATAATAAGATCATCACTATATGAATGTTGATCGTGTAACTAAGG 607
Db 4063 AATAATAATGTAATAATAATTGTATTATTATTATTATAGTCTACTTTATATAATATTA 4004

Qy 608 CAAGCTTAGGTTATATGAGCACCTTTTAGAGTGCTTTTATGGCGTGTGCTATGTTTGTG 667
Db 4003 TATTTATACATAATATACGTATATATAAAATTACATAATGGATTATATAGTATATATTA 3944

Qy 668 CTCGAGGTTGTAACCATCTTGAATAATAATAATAAGATCATGTTT 713
Db 3943 TATCAATAACATATGCATATATAATAACATTTATATTATATAGTCT 3898
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Search completed: June 23, 2006, 10:41:59
Job time : 115.753 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:12:55 ; Search time 980.107 Seconds
(without alignments)
8989.054 Million cell updates/sec

Title: US-10-728-051-2
Perfect score: 717
Sequence: 1 gctcacatagtagcc.....taaaagatcatgtttgtt 717

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	717	100.0	717	3	US-09-731-375A-2
2	717	100.0	717	9	US-10-728-323-2
3	717	100.0	717	9	US-10-728-051-2
4	717	100.0	717	10	US-10-899-551-3
5	474	66.1	474	6	US-10-228-806-3
6	474	66.1	474	6	US-10-100-303A-62
7	462	64.4	462	10	US-10-958-324-3
8	462	64.4	1162	10	US-10-958-324-1
9	80	11.2	80	10	US-10-958-324-7
10	65.6	9.1	1013	8	US-10-424-599-26383
11	63.4	8.8	770	7	US-10-302-633-1
12	62	8.6	62	10	US-10-958-324-8
13	59.2	8.3	477	10	US-10-508-263-43
14	54.4	7.6	468	10	US-10-508-263-41
15	54.4	7.6	883	8	US-10-424-599-121530
16	51.4	7.2	5392	16	US-11-224-807-6
17	49.8	6.9	62658	8	US-10-322-281-420

c 18	49.6	6.9	454	4	US-09-925-065A-566559	Sequence 566559,
c 19	49.6	6.9	454	4	US-09-925-065A-566560	Sequence 566560,
c 20	49.6	6.9	454	5	US-09-925-065A-566559	Sequence 566559,
c 21	49.6	6.9	454	5	US-09-925-065A-566560	Sequence 566560,
c 22	49.6	6.9	52216	3	US-09-747-810-1	Sequence 1, Appli
c 23	49.6	6.9	169739	8	US-10-450-826-93	Sequence 93, Appli
c 24	49	6.8	349	8	US-10-424-599-133074	Sequence 133074,
c 25	49	6.8	62001	8	US-10-316-459-13	Sequence 13, Appli
c 26	48.2	6.7	7758	7	US-10-311-455-1076	Sequence 1076, Ap
c 27	48	6.7	6509	7	US-10-311-455-199	Sequence 199, App
c 28	47.8	6.7	1237	6	US-10-027-632-122633	Sequence 122633,
c 29	47.8	6.7	1237	7	US-10-027-632-122633	Sequence 122633,
c 30	47.6	6.6	451	8	US-10-424-599-24494	Sequence 24494, A
c 31	47.4	6.6	325	8	US-10-424-599-76496	Sequence 76496, A
c 32	46.4	6.5	945	12	US-10-301-480-585566	Sequence 585566,
c 33	46.4	6.5	945	12	US-10-301-480-1198975	Sequence 1198975,
c 34	46.2	6.4	1325	4	US-09-925-065A-19652	Sequence 19652, A
c 35	46.2	6.4	1325	5	US-09-925-065A-19652	Sequence 19652, A
c 36	46.2	6.4	1325	12	US-10-301-480-120889	Sequence 120889,
c 37	46.2	6.4	1325	12	US-10-301-480-734298	Sequence 734298,
c 38	46	6.4	686	4	US-09-925-065A-940622	Sequence 940622,
c 39	46	6.4	686	5	US-09-925-065A-940622	Sequence 940622,
c 40	45	6.4	1089	10	US-10-956-157-107	Sequence 107, App
c 41	46	6.4	1089	10	US-10-956-157-5342	Sequence 5342, App
c 42	45.6	6.4	6063	7	US-10-240-453-267	Sequence 267, App
c 43	45.4	6.3	5823	7	US-10-240-453-256	Sequence 256, App
c 44	45.2	6.3	611	4	US-09-925-065A-500442	Sequence 500442,
c 45	45.2	6.3	611	5	US-09-925-065A-500442	Sequence 500442,

ALIGNMENTS

RESULT 1

US-09-731-375A-2

; Sequence 2, Application US/09731375A

; Publication No. US20030035810A1

; GENERAL INFORMATION:

; APPLICANT: Caplan, Michael

; TITLE OF INVENTION: Microbial Delivery System

; FILE REFERENCE: 2002834-0100

; CURRENT APPLICATION NUMBER: US/09/731,375A

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 60/195,035

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Atachis hypogaea

US-09-731-375A-2

Query Match 100.0%; Score 717; DB 3; Length 717;

Best Local Similarity 100.0%; Pred. No. 5.4e-177;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GCTCACCCTACTAGTAGCCCTCGCCCTTTCTCTCTCGTCCCGCCACGCATCTCGAGGCA	60
Db	1	GCTCACCCTACTAGTAGCCCTCGCCCTTTCTCTCTCGTCCCGCCACGCATCTCGAGGCA	60
Qy	61	GCAGTGGGAACCTCCAAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG	120
Db	61	GCAGTGGGAACCTCCAAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG	120
Qy	121	GCCTCGAGAGCAACATCTTCATGAGAAATCCAACTGACGAGGATTCATATGAAACGGGA	180
Db	121	GCCTCGAGAGCAACATCTTCATGAGAAATCCAACTGACGAGGATTCATATGAAACGGGA	180
Qy	181	CCCGTACAGCCCTAGTCAGGATCCGCTACAGCCCTAGTCATATGATCGGAGAGCCCTGG	240
Db	181	CCCGTACAGCCCTAGTCAGGATCCGCTACAGCCCTAGTCATATGATCGGAGAGCCCTGG	240

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QY 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGNAACAACCAAG 300
|
|
|
DB 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGNAACAACCAAG 300
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|
QY 301 GTGCATGTGGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
|
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|
DB 301 GTGCATGTGGAGGCATTGCAACAGATCATGGAGAACCCAGAGCGATAGGTTGCAGGGGAG 360
|
|
|
QY 361 GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGAACTTGCCTCAACAGTGGCGGCTTAG 420
|
|
|
DB 361 GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGAACTTGCCTCAACAGTGGCGGCTTAG 420
|
|
|
QY 421 GGCAACACAGCGTTGGACCTTGGAAGTTCGAAAGTGGCGGAGAGAGATCTAAACACC 480
|
|
|
DB 421 GGCAACACAGCGTTGGACCTTGGAAGTTCGAAAGTGGCGGAGAGAGATCTAAACACC 480
|
|
|
QY 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATAGCTTATTTATCTATG 540
|
|
|
DB 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATAGCTTATTTATCTATG 540
|
|
|
QY 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTGA 600
|
|
|
DB 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTGA 600
|
|
|
QY 601 ACTAAGGCAAGCTTAGGTTATATAGGACCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
|
|
|
DB 601 ACTAAGGCAAGCTTAGGTTATATAGGACCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
|
|
|
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 717
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|
|
DB 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 717
|
|
|
RESULT 2
US-10-728-323-2
; Sequence 2, Application US/10728323
; Publication No. US2004020894A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0232
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-323-2
Query Match 100.0%; Score 717; DB 9; Length 717;
Best Local Similarity 100.0%; Pred. No. 5.4e-177;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGAGGCA 60
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|
|
DB 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGAGGCA 60
|
|
|
QY 61 GCAGTGGGAATCTCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
|
|
|
DB 61 GCAGTGGGAATCTCAAGGAGACAGAAGATGCCAGAGCCAGCTCGAGAGGCGCAACCTGAG 120
|
|
|
QY 121 GCCTCGGAGCAACATCTCATGAGAGAGATCCAAAGTGGAGAGATTTCATATCAACGGGA 180
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DB 121 GCCCTGCGAGCAACATCTCATGAGAGATCCAAAGTGGAGAGGATTCATATGAAACGGA 180
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|
QY 181 CCGGTACAGCCCTAGTACAGGATCCGTTACAGCCCTAGTCCATATGATCGGAGAGGCCCTGG 240
|
|
|
DB 181 CCGGTACAGCCCTAGTACAGGATCCGTTACAGCCCTAGTCCATATGATCGGAGAGGCCCTGG 240
|
|
|
QY 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGNAACAACCAAG 300
|
|
|
DB 241 ATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGNAACAACCAAG 300
|
|
|
QY 301 GTGCATGTGGAGGCATTGCAACAGATCATGAGAAACCCAGAGCGATAGGTTGCAGGGGAG 360
|
|
|
DB 301 GTGCATGTGGAGGCATTGCAACAGATCATGAGAAACCCAGAGCGATAGGTTGCAGGGGAG 360
|
|
|
QY 361 GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGAACTTGCCTCAACAGTGGCGGCTTAG 420
|
|
|
DB 361 GCAACAGGAGCAACAGTTCAGAGGGAGCTCAGAACTTGCCTCAACAGTGGCGGCTTAG 420
|
|
|
QY 421 GGCAACACAGCGTTGGACCTTGGAAGTTCGAAAGTGGCGGAGAGAGATCTAAACACC 480
|
|
|
DB 421 GGCAACACAGCGTTGGACCTTGGAAGTTCGAAAGTGGCGGAGAGAGATCTAAACACC 480
|
|
|
QY 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATAGCTTATTTATCTATG 540
|
|
|
DB 481 TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATAGCTTATTTATCTATG 540
|
|
|
QY 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTGA 600
|
|
|
DB 541 GTTATGTTTAGTTTGGTAAATAAAGATCATCACTATATGAATGTGTTGATCGTGTGA 600
|
|
|
QY 601 ACTAAGGCAAGCTTAGGTTATATAGGACCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
|
|
|
DB 601 ACTAAGGCAAGCTTAGGTTATATAGGACCTTTAGAGTGCCTTTATGGCGTGTCTATGT 660
|
|
|
QY 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 717
|
|
|
DB 661 TTTGTTGCTGCAGAGTTGTAACCATCTTGAATAATATAAAAAAGATCATGTTTTGTT 717
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|
|
RESULT 3
US-10-728-051-2
; Sequence 2, Application US/10728051
; Publication No. US20040234548A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0222
; CURRENT APPLICATION NUMBER: US/10/728,051
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-051-2
Query Match 100.0%; Score 717; DB 9; Length 717;
Best Local Similarity 100.0%; Pred. No. 5.4e-177;
Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGAGGCA 60
|
|
|
DB 1 GCTCACCATACTAGTAGCCCTCGCCCTTTTCTCTCGCTGCCCGCCGATCTCGAGGCA 60
|
|
|
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Db	1	GCTCACCATACTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCCA	CGCATCTGCGAGGCA	60
Qy	61	GCAGTGGGAACTCCAAAGGAGACAGAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTTGAG	120	
Db	61	GCAGTGGGAACTCCAAAGGAGACAGAAGATCCAGAGCCAGCTCGAGAGGCGCAACCTTGAG	120	
Qy	121	GCCCTGGAGCAACATCTCATGCAAGAATGCCAACGTGACGAGGATTCATATGACCGGGA	180	
Db	121	GCCCTGGAGCAACATCTCATGCAAGAATGCCAACGTGACGAGGATTCATATGACCGGGA	180	
Qy	181	CCCGTACAGCCCTAGTCAAGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTGG	240	
Db	181	CCCGTACAGCCCTAGTCAAGATCCGTACAGCCCTAGTCCATATGATCGAGAGGCGCTGG	240	
Qy	241	ATCCTCTCAGCAACAGAGAGGTGTTGCAATAGAGCTGAAACAGGTTTGAGAACCAACAAAG	300	
Db	241	ATCCTCTCAGCAACAGAGAGGTGTTGCAATAGAGCTGAAACAGGTTTGAGAACCAACAAAG	300	
Qy	301	GTGCGATGTGGAGGCATTGCAACAGATCATGAGAACCCAGAGCGATAGGTTGCAGGGGAG	360	
Db	301	GTGCGATGTGGAGGCATTGCAACAGATCATGAGAACCCAGAGCGATAGGTTGCAGGGGAG	360	
Qy	361	GCAACGAGGCAACAGGTTCAAGAGGGAGCTCAGGAAGCTTCGCTCAACAGTTCGCGCTTAG	420	
Db	361	GCAACGAGGCAACAGGTTCAAGAGGGAGCTCAGGAAGCTTCGCTCAACAGTTCGCGCTTAG	420	
Qy	421	GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	480	
Db	421	GGCACACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGAGACAGATCTAAACACC	480	
Qy	481	TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATATAAGCTATTATCTATG	540	
Db	481	TATCTCAAAAAAGAAAAAGAAAAAGAAAAATAGCTTATATATAAGCTATTATCTATG	540	
Qy	541	GTTATGTTTGTAGTTTGTGTAATAAAGATCATCACTATATGAATGTTGATCGTGTA	600	
Db	541	GTTATGTTTGTAGTTTGTGTAATAAAGATCATCACTATATGAATGTTGATCGTGTA	600	
Qy	601	ACTAAGGCAAGCTTAGGTTATATAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTATGT	660	
Db	601	ACTAAGGCAAGCTTAGGTTATATAGCACCTTTAGAGTGCTTTTATGGCGTTGTCTATGT	660	
Qy	661	TTTGTTCTCGAGGTTGTAACCATCTTGAAATAATAAAAAAGATCATGTTTGT	717	
Db	661	TTTGTTCTCGAGGTTGTAACCATCTTGAAATAATAAAAAAGATCATGTTTGT	717	
RESULT 5				
US-10-228-806-3				
; Sequence 3, Application US/10228806				
; Publication No. US20030049237A1				
; GENERAL INFORMATION:				
; APPLICANT: Bannon, et al.				
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions				
; TITLE OF INVENTION: to Allergy				
; FILE REFERENCE: 2002834-0043				
; CURRENT APPLICATION NUMBER: US/10/228,806				
; CURRENT FILING DATE: 2002-08-26				
; NUMBER OF SEQ ID NOS: 81				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 3				
; LENGTH: 474				
; TYPE: DNA				
; ORGANISM: Arachis hypogaea				
; US-10-228-806-3				
Query Match 66.1%; Score 474; DB 6; Length 474;				
Best Local Similarity 100.0%; Pred. No. 2e-113;				
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	2	CTACCATACTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG	61	
Db	1	CTACCATACTAGTAGCCCTCGCCCTTTCTCTCTGCTGCCACGCATCTGCGAGGCGAG	60	

QY 62 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCAGAGGGCGAACTTGAGG 121
DB |||||
61 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCAGAGGGCGAACTTGAGG 120
QY 122 CCTGCGAGCAACATCTCATGCAAGAGATCCACGTCGACGAGATTCATATGAACGGAC 181
DB |||||
121 CCTGCGAGCAACATCTCATGCAAGAGATCCACGTCGACGAGATTCATATGAACGGAC 180
QY 182 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGGA 241
DB |||||
181 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGGA 240
QY 242 TCCTCTCAGCAACAGAGAGGTGTCATGAGCTGAACTGAACTGAGAACTGAGAACTGAGG 301
DB |||||
241 TCCTCTCAGCAACAGAGAGGTGTCATGAGCTGAACTGAGAACTGAGAACTGAGG 300
QY 302 TGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAGG 361
DB |||||
301 TGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAGG 360
QY 362 CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAGG 421
DB |||||
361 CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAGG 420
QY 422 GCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGACAGACTATAA 475
DB |||||
421 GCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGACAGACTATAA 474

RESULT 6

US-10-100-303A-62
; Sequence 62, Application US/10100303A
; Publication No. US20030202980A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction
; FILE REFERENCE: to Allergy
; CURRENT APPLICATION NUMBER: US/10/100,303A
; PRIOR FILING DATE: 2002-03-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 62
; TYPE: DNA
; ORGANISM: Arachis hypogaea, Prot/Nucleo Ara h 2
US-10-100-303A-62

Query Match 66.1%; Score 474; DB 7; Length 474;
Best Local Similarity 100.0%; Pred. No. 2e-113;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCACCATCTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGATCTCGAGGCGAG 61
DB |||||
1 CTCACCATCTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGATCTCGAGGCGAG 60
QY 62 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAGG 121
DB |||||
61 CAGTGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAGG 120
QY 122 CCGTGCAGCAACATCTCATGCAAGATCCACGTCGACGAGATTCATATGAACGGGAC 181
DB |||||
121 CCGTGCAGCAACATCTCATGCAAGATCCACGTCGACGAGATTCATATGAACGGGAC 180
QY 182 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGGA 241
DB |||||
181 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGGA 240
QY 242 TCCTCTCAGCAACAGAGAGGTGTCATGAGCTGAACTGAGTTGAGAACTGAGG 301
DB |||||
241 TCCTCTCAGCAACAGAGAGGTGTCATGAGCTGAACTGAGTTGAGAACTGAGG 300

QY 302 TGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAGG 361
DB |||||
301 TGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAGG 360
QY 362 CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAGG 421
DB |||||
361 CAACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAGG 420
QY 422 GCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGACAGACTATAA 475
DB |||||
421 GCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAGACAGACTATAA 474

RESULT 7

US-10-958-324-3
; Sequence 3, Application US/10958324
; Publication No. US20050114924A1
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: AKNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIOUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/10/958,324
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 682
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-958-324-3

Query Match 64.4%; Score 462; DB 10; Length 682;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCACCATCTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGATCTCGAGGCA 60
DB |||||
67 GCTCACCATCTAGTAGCCCTCGCCCTTTTCCTCTCGCTGCCACGCGATCTCGAGGCA 126
QY 61 GCAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAG 120
DB |||||
127 GCAGTGGGAACTCCAAGGAGACAGAAAGATGCCAGAGCCAGCTCGAGAGGGCGAACTTGAG 186
QY 121 GCCTCGAGCAACATCTCATGCAAGATCCAACTGACGAGATTCATATGAACGGGA 180
DB |||||
187 GCCTCGAGCAACATCTCATGCAAGATCCAACTGACGAGATTCATATGAACGGGA 246
QY 181 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGG 240
DB |||||
247 CCGTACAGCCCTAGTCAGGATCCGTCAGCCCTAGTCCATATGATCGGAGGCGCTGG 306
QY 241 ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACTGAGG 300
DB |||||
307 ATCCTCTCAGCAACAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACTGAGG 366
QY 301 GTGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAG 360
DB |||||
367 GTGCATGTCGAGGCAATGCAACAGATCATGGAAACAGAGCGATAGGTTGCAGGGGAG 426
QY 361 GCACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAG 420
DB |||||
427 GCACAGGAGCAACAGTTCAAGAGGAGCTCAGGAACCTTGCTCAACAGTCGGCGCTTAG 486
QY 421 GGCACCAACAGCGTTGCGACTTGGACGTCGAAAGTGGCGGAG 462
DB |||||

[Handwritten signature]


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136 GCAGCACCAGCAAGA---TAGTGCCTCCAGAGAGCTCCAGGGGTGAACCTCAGCCCTG 192
127 CGAGCAACATCTCATGAGAAATCAACCGTGAAGAGGATTCATATGAACGGGACCCGTA 186
193 CGAGAGCACATCATGAGAAATCAACGGCCGCGGATGACGATGATGATGATGATGATGAT 252
187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTAGTCCATATATGCGAG----- 231
253 CGACAATCACTCTCAGGACCATGCGGGGAGAAATCACTACATGAAGGAGCAAGG 312
232 -----AGGCGCTGGATCTCTCAGCACCAAGAGAGGTGTTCAATGAGCTGACCA 282
313 AAAAGCAGAGCAAGAAAGAAAGACATGACAGAGTGTCTGCACAGAAATGAGCGA 372
283 GTTTGAGAAACAACAAAGGTGTCATGTCGAGGCAATTCGAACAGATCATGAGAACACAGAG 342
373 GCT---GAGNAGCCCCAATGCCAGTGCAGAGCGCTGCAGAAATATGGAGAACACAGAG 429
343 CGATAGGTTGACGGGAGGCAACAGGAGCAACAGTTCAAGAGGGAGCTCAGGAATTTGCC 402
430 CGAGGAATCTGGAGAGAGCAGAAAGAAAGAA---ATGGAGAGGAGCTCATTAACCTTGGC 486
403 TCACAGTGGCGCTTAGGCGACACACAGCGTTGGAGCTTGGAGCTCGAAGTGGCGCAG 462
487 TACTATGTGAGGTTTGGACCCATGATCCAGTGGAGCTTGTCTCCGA-----TGACTA 540
463 AGACAGATCTAAACACCTATCTCAAAAAAGAAAGAAAGAAAGAAATAGCTTATA 522
541 AGAAGTTAAAGCAATGTTGCTACTTGTAGTACTAACACATGATGATAGTTATGCT 600
523 TATAAGCTATATCTATGTTATGTTTGGTAAATTAATAAGATCATCACTATATG 582
601 AGCTAGCTATAACATAAGCTGTCTGAGTGTGTGTATATTAATAAAGATCATCACTGG 660
583 AATGTTGATCGGTGTTAACTAAGGCAAGCTTAGTTATATGAGCACTTTAGAGTGCTT 642
661 TGAATGGTATCGTGTACGTCACCTACTTAGTAGGCAATGGAAGCACTTAGAGTGTGCTT 720
643 T---TATGGGTTGTCTATCTTTTGTGTCGAGAGTTGTAACCATCTTTGAAAT 693
721 TGTGCATGGCTTGCCTCTGTTTGAGACITTTTGTAAATGTTTCGAGTTTAAAT 774

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RESULT 11
US-10-302-633-1
; Sequence 1, Application US/10302633
; Publication No. US20030229038A1
; GENERAL INFORMATION:
; APPLICANT: de Lumen, Benito O.
; Galvez, Alfredo F.
; TITLE OF INVENTION: Lunasin Peptides
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10302,633
; FILING DATE: 22-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/531,727
; FILING DATE: 21-Mar-2000
; APPLICATION NUMBER: 08/938,675

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; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B98-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-302-633-1

Query Match      8.8%; Score 63.4; DB 7; Length 770;
Best Local Similarity 51.6%; Pred. No. 9e-06;
Matches 369; Conservative 0; Mismatches 301; Indels 45; Gaps 8;

QY 7 CATACTAGTAGCCCTCGCCCTTTTCCTCCTCGTCCACGATCTTCGAGGCGAGCAGTG 66
Db 28 CACAATCCTCCTCATCTCTCTCTCTTCGTCATCGCCACACTTTCGAGCGCCTCCAAATG 87
QY 67 GGAATCTCAAGGAGCAGAAAGATGCCAGAGCCAGCTTCGAGAGGGCGAACTGAGGCCCTG 126
Db 88 GCAGCACACGCAAGA---TAGCTGCCGCAAGCAGCTCCAGGGGTGAACCTCACGCCCTG 144
QY 127 CGAGCAACATCTCATGCAAGATCCAACTGACGAGGATTCATATGAACGGGACCCGTA 186
Db 145 CGAAGAGACATCATGGAAGATCCAAAGCCGCGCGATGACGATGATGATGATGATGATGAT 204
QY 187 CAGC-----CCTAGTCAGGATCCGTACAGCCCTTAGTCCATATGATCGAG- 231
Db 205 CGACAATCACATCTCTCAGGACCATGCGGGAAGAAATCAACTACATAAGGAGGAACGAAG 264
QY 232 -----AGGCGCTGGATCTCTCAGCACCAAGAGAGGTGTTGCAATGAGCTGACGA 282
Db 265 AAAAGCAGAAAGCAAGAAAGAAAGACACATGCAAGAGTGTCTGCACAGAAATGAGCGA 324
QY 283 GTTTGAGAAACAACAAAGGTGCAATGTCGAGGCAATTCGAACAGATCATGAGAACACAGAG 342
Db 325 GCT---GAGAAGCCCCCAATGCCAGTGCAGAGCGCTGCAGAGATTAATGGAGAACACAGAG 381
QY 343 CGATAGGTTGCGAGGGAGGCAACAGAGCAACAGTTCAAGAGGGAGCTCAGGAACCTTGCC 402
Db 382 CGAGGAATCGGAGGAGCAAGCAGAAAGAAAGAA---ATGGAGAGGAGCTCATTAACCTTGGC 438
QY 403 TCAACAGTGGCGCTTAGGGCACCAAGCGTTCCGACTTGGAGCTGCA-AAGTGGCGGCA 461
Db 439 TACTATGTGCAAGGTTTGGACCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 498
QY 462 GAGACAGATCTAAACACACCTATCTCAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAT 521
Db 499 TAAAAGCAATGTTGTCATCTGTCGTAACATGATGATGATGATGATGATGATGATGATGATGATGAT 555
QY 522 ATATAAGCTATTATCTATGTTATGTTTATGTTTGGTAAATAATAAGATCATCACTATAT 581
Db 556 -----AGCTATAACATAAGCTGCTCTGAGTGTGTTGTTATATTAAATAAGATCATCACTG 610
QY 582 GAATGTTGATCGTGTAACTAAGCAAGCTTAGTTATATAGCACCTTTAGAGTGCT 641
Db 611 GTGAATGGTATCGTGTACGTACCTTACTTTAGTAGGCAATGGAAGCACCTTAGAGTGCT 670
QY 642 TT---TATGGCGTTGCTATGTTTGTGTCGAGAGTTGTAACCATCTTTGAAAT 693
Db 671 TTGTGATGGCCTTGCTCTGTTTGTAGACTTTTGTAAATGTTTCGAGTTTAAAT 725

RESULT 12
US-10-958-324-8

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QY	127	CGAGCAACATCTTCATGCAGAAAGATCCACGTCGACGAGGATTCATATGACCGGACCCGTA	188
DB	129	CGAAGACGACATCATGGAGAAAGATCCAAAGCCCGCGCATGACGATGATGATGACGA	188
QY	187	CAGC-----CCTAGTCAGGATCCGTACAGACCCCTAGTCCATATGATCGAG-----	231
DB	189	CGACAATCATCTCTCAGGACCATGCGGGGAAGATCAACTACATAAGGAGGAACGAAGG	248
QY	232	-----AGCGCTGGATCTCTTCAGCACACCAGAGAGGTTGTCATAGCTGAACGA	282
DB	249	AAAAGACGAAGACGAAGAAGAACACATGTCAGAAGTGTCTGCACAGAAATGAGCGA	308
QY	283	GTTTGGAGAACAAACCAAGAGTGTCATGTCGAGGCAATTCACACAGATCATGGAGAACGAG	342
DB	309	GCT---GAGAAGCCCCAAATGCCAGTGCAAAGCGCTGCAGAAGATATGGAGAACGAG	365
QY	343	CGATAGGTTGACGGGAGGCAACAGGAGCAACAGTTCACAGAGGAGCTCAGGAACTTGCC	402
DB	366	CGAGGAACCTGGAGAGAACGCAAGAAGAAA---ATGAGAGAGGAGCTCATTAACCTGGC	422
QY	403	TCAACAGTGGCGCTTTAGGSCACCACAGCGCTTGCGACTTTGAGCGTCGA	450
DB	423	TACTATGTGCAGGTTTGGACCCATGATCCAGTGGCACTTGTCTCTCCGA	470

RESULT 14
 US-10-508-263-41
 ; Sequence 41, Application US/10508263
 ; Publication No. US20050260754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BASF Plant Science GmbH
 ; TITLE OF INVENTION: Constructs and methods for regulating gene expression
 ; FILE REFERENCE: 53262-20085.00
 ; CURRENT APPLICATION NUMBER: US/10/508,263
 ; CURRENT FILING DATE: 2004-09-20
 ; NUMBER OF SEQ ID NOS: 126
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 468
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(465)
 ; OTHER INFORMATION: 2S albumins 1
 US-10-508-263-41

Query Match	7.8%;	Score 54.4;	DB 10;	Length 468;
Best Local Similarity	61.5%;	Pred. No. 0.0016;		
Matches 123;	Conservative 0;	Mismatches 71;	Indels 6;	Gaps 2;

QY	251	CACCAAGAGAGGTTGTCATGAGCTGAACGAGTTTGAGAACACCAAGGTGCATGTGC	310
DB	268	CACATCGAAGTGTCTGACGCGAAATGAGCGAGCT---GAAAAGCCCATATGCCAGTGC	324
QY	311	GAGGCAATGCAACAGATCATGGAGAACCAAGAGCATAGGTTGACGGGAGGCAACAGAG	370
DB	325	AAAGCCCTACAGAAATATGGATACCAGAGCGAGCACTGGAGGGAGGAGGAAGAAG	384
QY	371	CAACAGTTCAAGAGGAGGCTCAGGAATCTGCCTCAACAGCTGCGGCCCTTTAGGGCACACAG	430
DB	385	---CAGATCGAGAGAGAGCTCATGAACCTTGGCTATTAGGTGCAGGTTGGGACCCCATGATA	441
QY	431	CGTTGCGACTTGCAGCTCGA	450
DB	442	GGGTGCGACTTGTCTCTCCGA	461

RESULT 15
 US-10-424-599-121530
 ; Sequence 121530, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:21:18 ; Search time 15.6052 Seconds
(without alignments)
11014.453 Million cell updates/sec

Title: US-10-728-051-2

Perfect score: 717

Sequence: 1 gctcaccatactagtagcc.....taaaagatcatgttttgg 717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New*

- 1: /EMC_Celerra_SID33/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 2: /EMC_Celerra_SID33/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 3: /EMC_Celerra_SID33/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 4: /EMC_Celerra_SID33/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 5: /EMC_Celerra_SID33/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 6: /EMC_Celerra_SID33/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 7: /EMC_Celerra_SID33/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 8: /EMC_Celerra_SID33/ptodata/1/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.4	7.6	714	US-10-953-349-13196	Sequence 13196, A
2	43.2	6.0	8172	US-10-517-441-717	Sequence 717, App
3	43	6.0	8172	US-10-517-441-443	Sequence 443, App
4	41.8	5.8	56580	US-10-553-298-1	Sequence 1, Appli
5	41	5.7	226	US-10-471-571A-969	Sequence 969, App
6	40.4	5.6	8391	US-11-217-529-166179	Sequence 166179, App
7	40.2	5.6	4857	US-10-517-441-697	Sequence 697, App
8	39.4	5.5	6521	US-10-517-441-309	Sequence 309, App
9	39.4	5.5	6521	US-10-517-441-583	Sequence 583, App
10	39	5.4	9859	US-10-517-441-730	Sequence 730, App
11	38.8	5.4	8900	US-10-517-441-428	Sequence 428, App
12	38.8	5.4	8900	US-10-517-441-702	Sequence 702, App
13	38.6	5.4	4857	US-10-517-441-423	Sequence 423, App
14	38.6	5.4	15355	US-10-517-441-415	Sequence 415, App
15	38.6	5.4	15355	US-10-517-441-689	Sequence 689, App
16	38.4	5.4	8172	US-10-517-441-718	Sequence 718, App
17	38	5.3	3107	US-10-517-441-401	Sequence 401, App
18	38	5.3	3107	US-10-517-441-675	Sequence 675, App
19	38	5.3	3501	US-10-517-441-499	Sequence 499, App
20	38	5.3	3501	US-10-517-441-773	Sequence 773, App
21	38	5.3	8172	US-10-517-441-99	Sequence 99, Appl
22	36.8	5.1	4857	US-10-517-441-423	Sequence 423, App
23	36.8	5.1	4857	US-10-517-441-697	Sequence 697, App
24	36.8	5.1	8172	US-10-517-441-444	Sequence 444, App
25	36.8	5.1	9353	US-10-517-441-735	Sequence 735, App

ALIGNMENTS

RESULT 1

US-10-953-349-13196
; Sequence 13196, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 13196
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-13196

Query Match 7.6%; Score 54.4; DB 6; Length 714;
Best Local Similarity 61.5%; Pred. No. 3.5e-05;
Matches 123; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

Qy	251	CACCAAGAGAGGTGTTGCAATGAGCTGAACGAGTTTGAGAACCAACCAAGTGTCATGTC	310
Db	294	CACATGCAGAGGTGCTGCAGCGAAATGAGCGAGCT--GAAAAAGCCCATATGCCAGTGC	350
Qy	311	GAGGCATTGCACAGATCATGGAGACCGAGCGATAGTTGCGAGGGGCAACAGAG	370
Db	351	AAAGCCCTACAGAAGATAATGGATAACCGAGCGCAACTGGAGGGGGAAGGAAG	410
Qy	371	CAACAGTTTCAAGAGGGAGCTTCAGCAACTTGCCTCAACAGTGCCTTAGGGCCACACAG	430
Db	411	---CAGATGGAGAGAGCTCATGAATCTGGCTATTAGTGCAGTTGGACCATGATA	467
Qy	431	CGTTGCGACTTGGACCTCGA	450
Db	468	GGGTGCGACTTGTCTCCGA	487

RESULT 2

US-10-517-441-717/c
; Sequence 717, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FORKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas

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; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 717
; LENGTH: 8172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-717

Query Match      6.0%; Score 43.2; DB 6; Length 8172;
Best Local Similarity 52.8%; Pred. No. 0.089;
Matches 93; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 438 ACTTGACGTCGAAGTGGCGGAGACAGACAGATACCTAAACACCTATCTCAAAAAAGAAA 497
Db 6974 AATTATACCCACACTCTAACTTAACAAAAATAAACTCCATCTCAAAAAAGAAA 6915

QY 498 AGAAAAAGAAAATAGCTTATATATAAGCTATTATCTATGTTATGTTTGG 557
Db 6914 AAAAAAAAATCAATTAATACTTTAAACTAAATTTATATAATTTTATCTTTTAAACA 6855

QY 558 TAATAATAAGATCATCATATATGAATGTGTGATCGTGAAGCTAAAGCAAGCT 613
Db 6854 TAAAAATAAAACATTTATTCTATAAAATTTACTAAAAATTAATTTATAAAATCACT 6799

RESULT 3
US-10-517-441-443/c
; Sequence 443, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FORKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; ;
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```
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 443
; LENGTH: 8172
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-443

Query Match      6.0%; Score 43; DB 6; Length 8172;
Best Local Similarity 55.8%; Pred. No. 0.1;
Matches 82; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 467 AGATACTAAACACCTATCTCAAAAAAGAAAAGAAAAGAAATAGCTTATATATA 526
Db 6945 AAAAAATAAACTCCGCTCAAAAAAGAAAAGAAAAGAAAATCAATTTAAATCTTTAA 6886

QY 527 AGCTATTATCTATGTTATGTTTGGTAATAATAAGATCATCATATATGAATG 586
Db 6885 CTAAATTTATTATAATTTTATCTTTTAAACAATAAAAAATAAACATTTTCTTATAAAT 6826

QY 587 TGTGTATCGTGTAACTAAGCAAGCT 613
Db 6825 TACTAAAAATTAATTTATAAAATACGCT 6799

RESULT 4
US-10-553-298-1
; Sequence 1, Application US/10553298
; Publication No. US20060110385A1
; GENERAL INFORMATION:
; APPLICANT: NeuroNova AG
; TITLE OF INVENTION: A Method for Diagnosing and Treating Affective Disorders
; FILE REFERENCE: XXX
; CURRENT APPLICATION NUMBER: US/10/553,298
; CURRENT FILING DATE: 2005-10-14
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 56580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon1
; LOCATION: (3000)..(3124)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon2
; LOCATION: (24841)..(25009)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon3
; LOCATION: (26134)..(26202)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon4
; LOCATION: (30958)..(31030)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon5
; LOCATION: (32481)..(32577)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon6
; LOCATION: (35416)..(35496)
; OTHER INFORMATION:
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;
; FEATURE:
; NAME/KEY: exon7
; LOCATION: (36113)..(36242)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon8
; LOCATION: (37541)..(37677)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon9
; LOCATION: (45470)..(45560)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon10
; LOCATION: (47229)..(47295)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon11
; LOCATION: (47380)..(47529)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon12
; LOCATION: (50438)..(50539)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: exon13
; LOCATION: (54392)..(54889)
; OTHER INFORMATION:
; US-553-298-1

Query Match      5.8%; Score 41.8; DB 6; Length 56580;
Best Local Similarity 59.8%; Pred. No. 0.5;
Matches 70; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 440 TTGACGCTCGAAGTGGCGGACAGACAGACTACTAAACACTATCTCAAAAAAGAAAG 499
    |||||
Db 5986 TTGCACCACCTGCACCTCAGCGCTGAGCCACAGACACTCTCTCAAAAAAGAAAG 6045
    |||||

Qy 500 AAAAGAAAAGAAATAGCTTATATAGCTATTAAGCTATTATCTATGTTAGTTTG 556
    |||||
Db 6046 AAAAGAAAAGAAATATATATATATATATATATATATATATATATATAGTTT 6102

RESULT 5
US-10-471-571A-969
; Sequence 969, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927NO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 969
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-10-471-571A-969

Query Match      5.7%; Score 41; DB 6; Length 276;
Best Local Similarity 63.9%; Pred. No. 0.07;
Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 492 AAGAAAAGAAAAGAAAAGAAATAGCTTATATAGCTTATCTATGTTAGTTAG 551
    |||||
Db 66 AGGAAAAGAAATGCAAGTAACAAGTTATTTATTTATAGCATTTCTTAGTAG 125
    |||||

Qy 552 TTTTGGTAATAAAGATCATCTATATGAATGTG 588
    |||||
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```
Db 126 TTTTGGTATTCATAAAATTTTATGCGCGCAAGAAATATG 162

RESULT 6
US-11-217-529-166179/c
; Sequence 166179, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166179
; LENGTH: 8391
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-166179

Query Match      5.6%; Score 40.4; DB 7; Length 8391;
Best Local Similarity 63.3%; Pred. No. 0.48;
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 488 AAAAGAAAAGAAAAGAAAAGAAATAGCTTATATATAGCTTATCTATGTTATGT 547
    |||||
Db 2951 AAATAGATAAGATAAGATAAGATAAGATATATATATATATATATATATATATATAT 2892
    |||||

Qy 548 TTAGTTTGGTAAATAAAGATCATCTATATGAAT 585
    |||||
Db 2891 ATTTTATATATATATATATATATATATATATATATATATATATATATATAGGAAAT 2854
    |||||

RESULT 7
US-10-517-441-697/c
; Sequence 697, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
```



```
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 730
; LENGTH: 9859
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-730

Query Match      5.4%; Score 39; DB 6; Length 9859;
Best Local Similarity 54.5%; Pred. No. 1.2;
Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 438 ACTTGGACGTCGAAGTGGCGGACAGACAGATCACTAAACACCTATCTCAAAAAAGAAA 497
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 498 AGAAAAAGAAAAAGCTATATATATAGCTATTATCTATGTTATGTTAGTTTGG 557
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 558 TAATAATAAGATCATCACTATA 580
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 558 TAATAATAAGATCATCACTATA 580
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 558 TAATAATAAGATCATCACTATA 580
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-517-441-428/c
; Sequence 428, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOSKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 730
; LENGTH: 9859
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-702/c
; Sequence 702, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOSKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 702
; LENGTH: 8900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-702
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; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 428
; LENGTH: 8900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-428

Query Match      5.4%; Score 38.8; DB 6; Length 8900;
Best Local Similarity 57.4%; Pred. No. 1.3;
Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 466 CAGTACTAAACACCTATCTCAAAAAAGAAAAGAAAAGAAATAGCTTATATAT 525
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 526 AAGCTATTATCTATGTTATGTTTGGTAATAATAAGATCATCACTATATGAAT 585
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RESULT 12
US-10-517-441-702/c
; Sequence 702, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOSKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOFELER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 702
; LENGTH: 8900
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-702

Query Match      5.4%; Score 38.8; DB 6; Length 8900;
Best Local Similarity 57.4%; Pred. No. 1.3;
Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
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GenCore version 5.1.9
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Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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VERSION BD107900.1 GI:23202718
KEYWORDS JP 2002501748-A/3.
SOURCE unidentified
ORGANISM unidentified sequences.
REFERENCE 1 (bases 1 to 1524)
AUTHORS Sosin,H., Banon,G.A., Jr,W.A.B. and Samphson,H.A.
TITLE Methods and reagents for decreasing allergic reactions
JOURNAL Patent: JP 2002501748-A 3 22-JAN-2002;
UNIVERSITY OF ARKANSAS, MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY
UNIVERSITY OF NEW YORK, HOWARD SOSIN
COMMENT OS Arachis L. (Peanut)
PN JP 2002501748-A/3
PD 22-JAN-2002
PF 29-JAN-1999 JP 2000529437
PR 31-JAN-1998 US 60/073283,13-FEB-1998 US 60/074590 PR
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27-AUG-1998 US 09/141220
PI HAWADO SOSIN,GARY A BANON,WESLEY A BIRX JR,HYU A SAMPTHON PC
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		Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;			
		Aeschynomeneae; Arachis.			
REFERENCE		1			
AUTHORS		Bannon, G.A., Burks, W.A., Caplan, M.J., Sampson, H. and Sosin, H.			
TITLE		Peptide antigens			
JOURNAL		Patent: WO 0140264-A 7 07-JUN-2001;			
		Panacea Pharmaceuticals, LLC (US); The University of Arkansas (US)			
		; MOUNT SINAI SCHOOL OF MEDICINE OF THE CITY UNIVERSITY OF NEW YORK			
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QY	361	CACGAGAGGTGACCGTTTCGATGAGGTGATCTCATTCGAGTTCACACCGGTGTGCT	420
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DB	421	TTCTGGCTCTACAAACGACCAACACTGATGTTGTTGCTGTTCTTACTGACACCAAC	480
QY	481	AACAACGACCAACAGCTTGATAGTTTCCCGAGGAGATTCAAATTTGGCTGGGAAACCGGAG	540
DB	481	AACAACGACCAACAGCTTGATAGTTTCCCGAGGAGATTCAAATTTGGCTGGGAAACCGGAG	540
QY	541	CAAGAGTTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT	600
DB	541	CAAGAGTTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT	600
QY	601	AGCCCATACAGCCGCAAGTCTAGCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
DB	601	AGCCCATACAGCCGCAAGTCTAGCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
QY	661	CAGCAGCGCCGAGAGAACGAGCAGGACAAAGAGAAAGAAACGAAAGTGGAAACATCTTC	720
DB	661	CAGCAGCGCCGAGAGAACGAGCAGGACAAAGAGAAAGAAACGAAAGTGGAAACATCTTC	720
QY	721	AGCGGCTTACCGCGGAGTTCTTGGAAACAGCCCTCCAGGTTCCAGCAGACAGATAGTG	780
DB	721	AGCGGCTTACCGCGGAGTTCTTGGAAACAGCCCTCCAGGTTCCAGCAGACAGATAGTG	780
QY	781	CAAAACCTTAGAGCGGAGACCGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGGA	840
DB	781	CAAAACCTTAGAGCGGAGACCGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGGA	840
QY	841	GGCCTCAGAAATCTTGAGCCCGAGATAGAAAGAGACGTCGCGCAAGAAAGAGGAAATACGAT	900
DB	841	GGCCTCAGAAATCTTGAGCCCGAGATAGAAAGAGACGTCGCGCGCAAGAAAGAGGAAATACGAT	900
QY	901	GAAGATCAATATCAATACGATGAAGAGGATAGAGCGGTGGCAGGGGAGCAGGCGAGG	960
DB	901	GAAGATCAATATCAATACGATGAAGAGGATAGAGCGGTGGCAGGGGAGCAGGCGAGG	960
QY	961	GGGAAATGGTATTGAAGAGACGATCTGCACCGCAAGTGTCTAAAAAGAACATTGGTAGAAAC	1020
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DB	1021	AGATCCCTTGACATCTTACAACCTCAAGCTGGTTTCACTCAAAACCTGCCAACGATCTCAAC	1080
QY	1081	CTTCTAATACTTAGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCA	1140
DB	1081	CTTCTAATACTTAGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCA	1140
QY	1141	TTGTTTGTGCTCACTTACAACCAACGACACAGCATCATATATCGATTGAGGGACCG	1200
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LOCUS		Arachis hypogaea arachin Ahv-4 mRNA, complete cds.	
DEFINITION		AY848698	
ACCESSION		AY848698.1	GI:57669860
VERSION			
KEYWORDS		Arachis hypogaea (peanut)	
SOURCE		Arachis hypogaea	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.	
REFERENCE		1 (bases 1 to 1902)	
AUTHORS		Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.2.	
TITLE		Isolation of peanut genes encoding arachins and conglutins by expressed sequence tags	
JOURNAL		Plant Sci. 169 (2), 439-445 (2005)	
REFERENCE		2 (bases 1 to 1902)	
AUTHORS		Yan, Y., Wang, L. and Huang, S.	
TITLE		cDNA clone of peanut seed storage protein gene	
JOURNAL		Unpublished	
REFERENCE		3 (bases 1 to 1902)	
AUTHORS		Yan, Y., Wang, L. and Huang, S.	
TITLE		Direct Submission	
JOURNAL		Submitted (03-DEC-2004) Department of Biology and Biotechnology, Sun Yat-sen University, Guangzhou, Guangdong 510275, China	
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RESULT 7
AF086821 LOCUS 1853 bp mRNA linear PLN 29-SEP-1999
DEFINITION Arachis hypogaea glycinin (Arah4) mRNA, complete cds.
ACCESSION AF086821
VERSION AF086821.1 GI:5712198
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 1853)
AUTHORS Kleber-Janke,T., Cramer,R., Appenzeller,U., Schlaak,M. and
Becker,W.M.
TITLE Selective cloning of peanut allergens, including profilin and 2S
albumins, by phage display technology
JOURNAL Int. Arch. Allergy Immunol. 119 (4), 265-274 (1999)
PUBMED 10474031
REFERENCE 2 (bases 1 to 1853)
AUTHORS Kleber-Janke,T.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1998) Biochemische und Molekulare Allergologie,
Forschungszentrum Borstel, Parkallee 22, Borstel 23845, Germany
Location/Qualifiers
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ORIGIN

Query Match 91.3%; Score 1391.2; DB 4; Length 1853;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 68; Indels 2; Gaps 2;

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RESULT 8

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Arachis hypogaea Gly1 (Gly1) mRNA, complete cds.

AF125192
AF125192.2 GI:9864776

Arachis hypogaea (peanut)

ORGANISM

Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 1590)
Jain, A.K. and Basha, S.M.
Molecular cloning of a glycinin-type peanut seed storage protein
Unpublished
Jain, A.K. and Basha, S.M.
Direct Submission
Submitted (02-FEB-1999) Plant Biotechnology, Florida A&M
University, 301 South Perry Paige Building, Tallahassee, FL 32307,
USA
3 (bases 1 to 1590)
Jain, A.K. and Basha, S.M.
Direct Submission
Submitted (22-AUG-2000) Plant Biotechnology, Florida A&M
University, 301 South Perry Paige Building, Tallahassee, FL 32307,
USA

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

Sequence update by submitter

On Aug 22, 2000 this sequence version replaced gi:5825430.

Location/Qualifiers

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DB 845 TGCAAAATCTTAAGAGGCGAGAACGAGAGTGAAGAAGAGGAGGCCATTGTGCACAGTGAGGG 904
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DB 905 GAGGCTTCAGAACTTTGAGCCAGATAGAAAGAGAGGTGCCGACGAAAGAGAGAAATACG 964
QY 899 ATCAAGATGAATATGAATACGATGAAGAGGATAGAAGGCTGGCAGGGGAAAGCAGAGGCA 958
DB 965 ATCAAGATGAATATGAATACGATGAAGAGGATAGAAGGCTGGCAGGGGAAAGCAGAGGCA 1024
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DB 1025 GGGGGAATGTTATTGAAGAGACGATCTGCACACAAAGTGTAAAAAGAAACATTGGTAGAA 1084
QY 1019 ACAGATCCCTGCATCTACAACTTCAAGCTGGTTCACTCAAAACTGCCAACGATCTCA 1078
DB 1085 ACAGATCCCTGCATCTACAACTTCAAGCTGGTTCACTCAAAACTGCCAACGATCTCA 1144
QY 1079 ACCTTCTAATACCTTAGGTGGTGGACCTTAGTCTGAATATGGAATATCTTACAGGAATG 1138
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DB 1505 GGGAGCAGCAGGAGGCTTAAAGAACAAACCCCTTCAAGTTCTTGGTTCCAGCTCTC 1564
QY 1499 AGCAGTCTCCGAGGCTGTGGCTTAA 1524
DB 1565 AACAGTCTCTCAGGGCTGTGGCTTGA 1590
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AV722686 1901 bp mRNA linear PLN 08-JUL-2005
LOCUS Arachis hypogaea arachin Ahy-2 mRNA, complete cds.
DEFINITION AY722686
ACCESSION AY722686.1 GI:52001220
VERSION
KEYWORDS
SOURCE
ORGANISM
Arachis hypogaea (peanut)
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
```


Aeschynomeneae; Arachis.
1 (bases 1 to 1901)
Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.
Isolation of peanut genes encoding arachins and conglutins by
expressed sequence tags
Plant Sci. 169 (2), 439-445 (2005)
2 (bases 1 to 1901)
Yan, Y., Wang, L. and Huang, S.
cDNA clone of peanut seed storage protein gene
Unpublished
3 (bases 1 to 1901)
Yan, Y., Wang, L. and Huang, S.
Direct Submission
Submitted (30-JUL-2004) Department of Biology and Biotechnology,
Sun Yat-sen University, Guangzhou, Guangdong 510275, China
Location/Qualifiers
1. .1901
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ORIGIN
Query Match 87.2%; Score 1329.4; DB 4; Length 1901;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 1448; Conservative 0; Mismatches 66; Indels 39; Gaps 4;
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QY 62 ATCGCATTTGAATCAGAGGGCGGTTACATTCAGACTTTGGAAACCCCAACCAACAGAGTTGCG 121
DB 160 ACCGCTTGAATCGGAGGGCGGTTACATTCAGACTTTGGAAACCCCAACCAACAGAGTTGCG 219
QY 122 AATGCGCGCGCTCGCCCTCTCGCTTAGTCTTCGCGCCCAACCGCCCTTCGTAGGCTT 191
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DB 460 GTCAACAGAAAGTGCAGCGTTTCAGTCAAGGTGATCTCAATTCAGTTCCTCCACCGGTGTTG 519
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RESULT 11

AY439332 1886 bp mRNA linear PLN 26-OCT-2003
Arachis hypogaea storage protein mRNA, complete cds.
AY439332
AY439332.1 GI:37789211

KEYWORDS

Arachis hypogaea (peanut)

Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eustosids 1; Fabales; Fabaceae; Papilionoideae;

Aeschynomeneae; Arachis.

1 (bases 1 to 1886)

Yang, H.-X., Wang, F. and Bi, Y.-P.

Cloning of Arachin complete cDNA Sequence

Unpublished

2 (bases 1 to 1886)

Yang, H.-X., Wang, F. and Bi, Y.-P.

Direct Submission

Submitted (17-OCT-2003) Jinan, Shandong 250100, China

Location/Qualifiers

1. .1886

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11. .1621

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CDS

ORIGIN

Query Match 86.7%; Score 1321.6; DB 4; Length 1886;
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QY 122 AATGCGCGCGCTCGCCCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCGCTT 181
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RESULT 13

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DEFINITION Arachis hypogaea allergen Arah3/Arah4 gene, complete cds.
ACCESSION AF510854
VERSION AF510854.1 GI:21314464
KEYWORDS
SOURCE Arachis hypogaea (peanut)
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 3825)
Viquez, O.M., Konan, K.N. and Dodo, H.W.
Genomic characterization of the major peanut allergen genes, Arah3
and/or Arah4
Unpublished
REFERENCE 2 (bases 1 to 3825)
Viquez, O.M., Konan, K.N. and Dodo, H.W.
Direct Submission
Submitted (09-MAY-2002) Food and Animal Sciences, Alabama A&M
University, Meridian Street, 4900, Normal, AL 35762, USA
FEATURES
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DB 1642 ATGGTGACAATTAATAATACATAACAGAGATTCAATTTGGCTGGGAACACGGAAGAG 1701
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QY 847 AGAATCTTGAGCCCGAGATAGAGAG-----ACGTGCCGACGAGAGAGAGAGAGAG 891
DB 1993 AGAATCTTGAGCCCGAGATAG 2052
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Qy	1134	-----	1133
Db	2353	ATACTATCATTTTTTAAGTATTAAATTTTAAATACTAATGCTATAAGAAATAAATGTTAAC	2412
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Qy	1426	TATGGCTCCAAAGGGAGAGCAAGGACGCTTAAGAACCAACACCCCTTCAAGTTCTTC	1485
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Db	2833	GTTCACCGCTTCAGCAGTCTCTGAGGGCTGTGGCTTAA	2871
RESULT 14			
AY722687			
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DEFINITION	Arachis hypogaea arachin Ahy-3	mRNA, complete cds.	PLN 08-JUL-2005
ACCESSION	AY722687		
VERSION	AY722687.1	GI:52001222	
KEYWORDS	.		
SOURCE	Arachis hypogaea (peanut)		
ORGANISM	Arachis hypogaea		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;		
TITLE	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;		
JOURNAL	Aeschynomeneae; Arachis.		
REFERENCE	1 (bases 1 to 1786)		
AUTHORS	Yan, Y.S., Lin, X.D., Zhang, Y.S., Wang, L., Wu, K. and Huang, S.Z.		
TITLE	Isolation of peanut genes encoding arachins and conglutins by		
JOURNAL	expressed sequence tags		
REFERENCE	Plant Sci. 169 (2), 439-445 (2005)		
	2 (bases 1 to 1786)		

AUTHORS Yan, Y., Wang, L. and Huang, S.
TITLE cDNA clone of peanut seed storage protein gene
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1786)
AUTHORS Yan, Y., Wang, L. and Huang, S.
TITLE Direct Submission
JOURNAL Sun Yat-sen University, Guangzhou, Guangdong 510275, China
FEATURES
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ORIGIN

Query Match 45.6%; Score 694.8; DB 4; Length 1786;
Best Local Similarity 70.6%; Pred. No. 3.5e-196;
Matches 1054; Conservative 0; Mismatches 297; Indels 141; Gaps 4;
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QY 722 GCGGCTTCAGCCGCGGAGTTCCTCGAAACAAGCCCTTCCAGGTTCAGCAGACACATAGTGC 781
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DEFINITION Arachis hypogaea trypsin inhibitor mRNA, partial cds.
ACCESSION AF487543
VERSION AF487543.1 GI:22135347
KEYWORDS Arachis hypogaea (peanut)
SOURCE Arachis hypogaea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 657)
Dodo,H.W., Viquez,O.M., Maleki,S.J. and Konan,K.N.
cDNA clone of a putative peanut (Arachis hypogaea L.) trypsin
inhibitor has homology with peanut allergens Ara h 3 and Ara h 4
J. Agric. Food Chem. 52 (5), 1404-1409 (2004)
14995153
2 (bases 1 to 657)
Dodo,H.W. and Viquez,O.M.
Direct Submission
Submitted (25-FEB-2002) Food and Animal Sciences, Alabama A&M
University, Meridian Street, 4900, Normal, AL 35762, USA

FEATURES

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CDS

ORIGIN

Query Match 34.1%; Score 519.2; DB 4; Length 657;
Best Local Similarity 93.4%; Pred. No. 1.2e-143; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 38;

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Db 617 AAGAGTTCTTAAGATACCGACCAACAGAGACAGCAAGAG 656

Search completed: June 23, 2006, 18:12:43
Job time : 8897.98 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2006, 09:14:45 ; Search time 679.077 Seconds
(without alignments)
15647.278 Million cell updates/sec

Title: US-10-728-051-3
Perfect score: 1524
Sequence: 1 cggcagcaaccggaggagaa.....ctccgagggtgtggcttaa 1524

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
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 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*
 - 14: Geneseqn2005s:*
 - 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1524	100.0	1524	2	Az06384 Peanut al
2	1524	100.0	1524	2	Az22280 Ara h 3 a
3	1524	100.0	1524	8	Abx70612 Peanut Ar
4	1524	100.0	1524	10	Adg27543 Peanut cD
5	1520.8	99.8	1524	4	Aas08540 DNA encod
6	1391.2	91.3	1855	4	Aaf90338 Peanut al
7	517.4	34.0	1446	2	Aav17567 Coding se
8	517.4	34.0	1446	6	Abss5193 Glycine m
9	517.4	34.0	1446	10	Adh89252 G. max gl
10	517.4	34.0	1446	12	Adg43987 G. max gl
11	517.4	34.0	1673	13	Adx12705 Plant ful
12	517.4	34.0	1689	13	Adx13956 Plant ful
13	517.4	34.0	1694	13	Adx14017 Plant ful
14	517.4	34.0	1697	13	Adx13008 Plant ful
15	515.8	33.8	1671	13	Adx13019 Plant ful
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17	513	33.7	1434	14	Adz47109 Soybean m
18	513	33.7	1458	14	Adz47103 N-termina

19	513	33.7	1488	2	AAV17565	Aav17565 Coding se
20	513	33.7	1488	6	ABS55191	Abss55191 Glycine m
21	513	33.7	1488	10	ADH89244	Adh89244 G. max gl
22	513	33.7	1488	12	ADG43979	Adg43979 G. max gly
23	513	33.7	1694	13	ADX13099	Adx13099 Plant ful
24	513	33.7	1716	13	ADX13981	Adx13981 Plant ful
25	513	33.7	1718	13	ADX13067	Adx13067 Plant ful
26	513	33.7	1721	13	ADX13095	Adx13095 Plant ful
27	513	33.7	1724	13	ADX14012	Adx14012 Plant ful
28	513	33.7	1724	13	ADX13038	Adx13038 Plant ful
29	513	33.7	1727	13	ADX13028	Adx13028 Plant ful
30	513	33.7	1727	13	ADX13049	Adx13049 Plant ful
31	513	33.7	1729	13	ADX13589	Adx13589 Plant ful
32	513	33.7	1730	13	ADX13558	Adx13558 Plant ful
33	513	33.7	1743	3	AAZ92638	Aaz92638 cDNA enco
34	511.4	33.6	1458	14	ADZ47107	Adz47107 C-termina
35	511.4	33.6	1729	13	ADX14009	Adx14009 Plant ful
36	505.6	33.2	1458	6	ABS55192	Abss55192 Glycine m
37	505	33.1	1746	4	AAV17536	Aav17536 Soybean g
38	504	33.1	1458	2	AAV17566	Aav17566 Coding se
39	504	33.1	1458	10	ADH89246	Adh89246 G. max gl
40	504	33.1	1458	12	ADG43981	Adg43981 G. max gl
41	504	33.1	1610	13	ADX13062	Adx13062 Plant ful
42	504	33.1	1610	13	ADX13060	Adx13060 Plant ful
43	504	33.1	1678	13	ADX13588	Adx13588 Plant ful
44	504	33.1	1679	13	ADX14013	Adx14013 Plant ful
45	504	33.1	1685	13	ADX13533	Adx13533 Plant ful

ALIGNMENTS

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AAZ06384	
ID	AAZ06384 standard; DNA; 1524 BP.
XX	
AC	AAZ06384;
XX	
DT	17-OCT-2003 (revised)
DT	09-NOV-1999 (first entry)
XX	
DE	Peanut allergen, Ara h 3.
XX	
KW	allergy; immune response; transgenic; allergen; epitope;
KW	immunoglobulin E; Ig E; binding site; peanut; ds.
XX	
OS	Arachis hypogaea.
XX	
FH	Key
CDS	Location/Qualifiers
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PD	05-AUG-1999.
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PF	29-JAN-1999; 99WO-US002031.
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PR	31-JAN-1998; 98US-0073283P.
PR	13-FEB-1998; 98US-0074590P.
PR	13-FEB-1998; 98US-0074624P.
PR	13-FEB-1998; 98US-0074633P.
PR	27-AUG-1998; 98US-00141220.
XX	
XX	(UYAR-) UNIV ARKANSAS.
PA	(UYNY) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
PA	(SOSI/) SOSIN H.
XX	
PI	Sosin H, Bannan GA, Burks AW, Sampson HA;
DR	WPI; 1999-479189/40.

QY	1501	CAGTCTCCGAGGGCTGTGGCTTAA	1524	Db	61	AATCGCRATTGAATCAGAGGGGGTTACATTGAGACTTGGNACCCCAACACACAGGAGTTC	120
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				Db	121	GAATGCGCGGGCTGCGCCCTCTCTCGCTTAGTCTCCTCGCGCAACCCCTTCGTAGGCCT	180
RESULT 3				QY	181	TTCTACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTTG	240
ABX70612				Db	181	TTCTACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTTG	240
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XX	AC	ABX70612;		Db	241	ATATTCCCTGGTTGTTCTTAGACACTATGAAGAGCCCTCACACAAAGTCTCGATCTCAG	300
XX	26-MAR-2003	(first entry)		QY	301	TCCCAAGACCAACCAAGAGCGTCTCCAAGGAGAGACCAAGGCAACAGCAACGAGATAGT	360
XX	Peanut Ara h3 cDNA sequence.			Db	301	TCCCAAGACCAACCAAGAGCGTCTCCAAGGAGAGACCAAGGCAACAGCAACGAGATAGT	360
KW	Peanut; ss; allergy; Ara h1; Ara h2; Ara h3; gene; IgE binding site;			QY	361	CACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAGTTCCCAACCGGTGTGCT	420
KW	anaphylactic food allergen; antiallergenic; vaccine; wound healing.			Db	361	CACCAGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAGTTCCCAACCGGTGTGCT	420
OS	Arachis hypogaea.			QY	421	TTCTGGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTTCTTCTTACTGACACCAAC	480
XX	WO200274250-A2.			Db	421	TTCTGGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTTCTTCTTACTGACACCAAC	480
XX	26-SEP-2002.			QY	481	AACAACGACCAACCGAGCTTGATTCAGTTCCCGAGGAGATTCAATTTGGCTGGGAAACGAGGAG	540
XX	18-MAR-2002; 2002WO-US009108.			Db	481	AACAACGACCAACCGAGCTTGATTCAGTTCCCGAGGAGATTCAATTTGGCTGGGAAACGAGGAG	540
XX	16-MAR-2001; 2001US-0276822P.			QY	541	CAAGAGTTCTTAAGGTACCAGCAACCAAGCAGCAACGAGCAAGGAGCAAGAGAGCTTACCATAT	600
PR	18-MAR-2002; 2002US-00276822.			Db	541	CAAGAGTTCTTAAGGTACCAGCAACCAAGCAGCAACGAGCAAGGAGCAAGAGAGCTTACCATAT	600
XX	(PANA-) PANACEA PHARM.			QY	601	AGCCCATACAGCCCGCAAAAGTCAGCCTTAGACAAGAGAGCGTGAATTTAGCCCTTCGAGGA	660
XX	Caplan M, Sosin H, Sampson H, Bannon GA, Burks WA, Cockrell G;			Db	601	AGCCCATACAGCCCGCAAAAGTCAGCCTTAGACAAGAGAGCGTGAATTTAGCCCTTCGAGGA	660
PI	Compadre CM, Connaughton C, Helm RM, King NE, Kopper RA, Maleki SJ;			QY	661	CAGCAGCGCGCAGAGAAACGAGCAGGACCAAGAAAGAAACCAAGAGTGGAAACATCTTC	720
PI	Rabjohn PA, Shin DS, Stanley JS;			Db	661	CAGCAGCGCGCAGAGAAACGAGCAGGACCAAGAAAGAAACCAAGAGTGGAAACATCTTC	720
DR	WPI; 2003-018765/01.			QY	721	AGCGGCTTACCGCGGAGTTCCCTGGACAGCCCTTCAGGTTTCAGCAGACAGAGATAGTG	780
DR	P-PSDB; ABU52484.			Db	721	AGCGGCTTACCGCGGAGTTCCCTGGACAGCCCTTCAGGTTTCAGCAGACAGAGATAGTG	780
XX	New modified anaphylactic food allergen, useful for preventing or			QY	781	CAAAACCTTAAGAGCGCAGAGCCGAGAGTGAAGAAAGAGGAGGCCATTGTGACAGTGAGGGGA	840
PT	treating allergic reactions associated with e.g. anaphylactic allergens.			Db	781	CAAAACCTTAAGAGCGCAGAGCCGAGAGTGAAGAAAGAGGAGGCCATTGTGACAGTGAGGGGA	840
PS	Example 16; Fig 68A; 300pp; English.			QY	841	GGCCTCAGAAATCTTGAGCCCGAGTGAAGAGAGAGCTGCCGACGAAGAGGAAATACGAT	900
XX	The invention relates to a modified anaphylactic food allergen has an			Db	841	GGCCTCAGAAATCTTGAGCCCGAGTGAAGAGAGAGCTGCCGACGAAGAGGAAATACGAT	900
CC	amino acid sequence that is substantially identical to that of natural			QY	901	GAAGATGAATATGAATACCATGAAGAGGATAGAAGCGTGGCAGGGGAAACGAGGAGG	960
CC	anaphylactic food allergen, except for a cysteine residue that has been			Db	901	GAAGATGAATATGAATACCATGAAGAGGATAGAAGCGTGGCAGGGGAAACGAGGAGG	960
CC	modified so that it cannot participate in the disulphide bond. The			QY	961	GGAAATGGTATTGAAGAGAGCGATCTGCACCGCAGAGTGCTAAAAAAGAAACATTGGTAGAAAC	1020
CC	modification may also comprise mutation of the IgE binding sites to			Db	961	GGAAATGGTATTGAAGAGAGCGATCTGCACCGCAGAGTGCTAAAAAAGAAACATTGGTAGAAAC	1020
CC	reduce allergenicity. Also included are: (1) a method of making a			QY	1021	AGATCCCTCGACATCTACAAACCTCAAGCTGGTTCACTCAAAACTGCCAAGTCTCAAC	1080
CC	modified anaphylactic food allergen; (2) a nucleotide molecule encoding			Db	1021	AGATCCCTCGACATCTACAAACCTCAAGCTGGTTCACTCAAAACTGCCAAGTCTCAAC	1080
CC	or for causing a site specific mutation in the modified anaphylactic food			QY	1081	CTTCTAATCTTAGTGGGCTTGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCA	1140
CC	allergen; (3) a transgenic plant or animal expressing the modified			Db	1081	CTTCTAATCTTAGTGGGCTTGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCA	1140
CC	anaphylactic food allergen; (4) a method of treating an individual by			QY	1141	TTGTTTGTGCTCACTACAAACCAACGACATCATATATCGATTGAGGGGACGG	1200
CC	reducing the clinical response to a natural anaphylactic food allergen;			Db			
CC	and an isolated fragment of peanut allergen Ara h 1. The modified						
CC	anaphylactic food allergen is useful for preventing or treating allergic						
CC	reactions associated with any natural allergen such as food, insect,						
CC	rubber or preferably anaphylactic allergens. It is also useful for						
CC	treating wounds in mammals such as bovine, canine, feline, caprine,						
CC	ovine, porcine, murine or equine species. The present sequence is a cDNA						
CC	encoding a peanut allergen (e.g. Ara h1, h2 or h3)						
XX	Sequence 1524 BP; 455 A; 390 C; 398 G; 281 T; 0 U; 0 Other;						
SQ	Query Match	100.0%;	Score 1524;	DB 8;	Length 1524;		
	Best Local Similarity	100.0%;	Pred. No. 0;				
	Matches 1524; Conservative	0;	Mismatches	0;	Indels	0;	Gaps
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Db	1	CGCAGCAACCGGAGGAGAACGGGTGCGCACTTCAGGCGCTCAATGCGCAGAGACCTGAC	60				
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Db	181	TTCTACTCCAA	TGCTCCCGAGGAGTCTTCATCCAGCAAGGAGGGATAC	TTTGGGTTG	240
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Db	241	ATA	TTCCCTGGTTGTCTTAGACACTATGAAGAGCCTCACACAAAGGTGCTGATCTCAG		300
Qy	301	TCCCAAGACCA	CCACAGAGCGTCTCCAAAGGAGAGCAAAAGCCAAAGCAAGCAAGAGATAGT		360
Db	301	TCCCAAGACCA	CCACAGAGCGTCTCCAAAGGAGAGCAAAAGCCAAAGCAAGCAAGAGATAGT		360
Qy	361	CACCAAGGTG	CACCGGTTTCGATGAGGGTGATCTCATTTGCACTTCCCAACCGGTGTGCT		420
Db	361	CACCAAGGTG	CACCGGTTTCGATGAGGGTGATCTCATTTGCACTTCCCAACCGGTGTGCT		420
Qy	421	TTCTGGCTCT	TACAAACGACACGACACTGATGTTGTTGCTGTTCTTCTTACTGACACCAAC		480
Db	421	TTCTGGCTCT	TACAAACGACACGACACTGATGTTGTTGCTGTTCTTCTTACTGACACCAAC		480
Qy	481	AACAACGACA	CCAGCTTGATCAGTTCCCGAGGAGATTCAAATTTGGCTGGGAACACGGAG		540
Db	481	AACAACGACA	CCAGCTTGATCAGTTCCCGAGGAGATTCAAATTTGGCTGGGAACACGGAG		540
Qy	541	CAAGAGTCTT	TAAGGTACACGACAAACAGCAGACAAAGCAGACGAAAGAGCTTTACCATAT		600
Db	541	CAAGAGTCTT	TAAGGTACACGACAAACAGCAGACAAAGCAGACGAAAGAGCTTTACCATAT		600
Qy	601	AGCCCATAC	AGCCCGAAAGTACGCTTAGCAAGAAAGAGCGTGAAATTTAGCCCTCGAGGA		660
Db	601	AGCCCATAC	AGCCCGAAAGTACGCTTAGCAAGAAAGAGCGTGAAATTTAGCCCTCGAGGA		660
Qy	661	CAGCAGCGC	GAGAGAACGAGCAGACAGAGAGAGAAACCAAGGTGGAACATCTTC		720
Db	661	CAGCAGCGC	GAGAGAACGAGCAGACAGAGAGAGAAACCAAGGTGGAACATCTTC		720
Qy	721	AGCGGCTTC	ACGCGGAGTTCCTGGAAACAGCCCTTCAGGTTGACGACAGACAGATAGTG		780
Db	721	AGCGGCTTC	ACGCGGAGTTCCTGGAAACAGCCCTTCAGGTTGACGACAGACAGATAGTG		780
Qy	781	CAAAACCTA	AGAGCGCAGACCGAGAGTGAAAGAGGGAGCCATTGTGACAGTGAGGGGA		840
Db	781	CAAAACCTA	AGAGCGCAGACCGAGAGTGAAAGAGGGAGCCATTGTGACAGTGAGGGGA		840
Qy	841	GGCCTCAGA	ATCTTGAGCCAGATAGAAAGAGAGCGTGCCGACCAAGAGGAATACGAT		900
Db	841	GGCCTCAGA	ATCTTGAGCCAGATAGAAAGAGAGCGTGCCGACCAAGAGGAATACGAT		900
Qy	901	GAAGATGA	ATATGAATACGATGAAGAGGATAGAGGCGTGCGCAGGGGAGCAGAGCAGG		960
Db	901	GAAGATGA	ATATGAATACGATGAAGAGGATAGAGGCGTGCGCAGGGGAGCAGAGCAGG		960
Qy	961	GGGAATGG	TATGAAGAGCGATCTGCGCCGCAAGTGCTTAAAGAAACATTTGGTAGAAC		1020
Db	961	GGGAATGG	TATGAAGAGCGATCTGCGCCGCAAGTGCTTAAAGAAACATTTGGTAGAAC		1020
Qy	1021	AGATCCCTG	ACATCTACACCCCTCAAGCTGTTCACTCAAACTGCAACGATCTCAAC		1080
Db	1021	AGATCCCTG	ACATCTACACCCCTCAAGCTGTTCACTCAAACTGCAACGATCTCAAC		1080
Qy	1081	CTTCTAATA	CTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGGAATGCA		1140
Db	1081	CTTCTAATA	CTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGGAATGCA		1140
Qy	1141	TTGTTTGTG	CTCACTAACAACGCAACAGCATCATATATCGATTGAGGGGACGG		1200
Db	1141	TTGTTTGTG	CTCACTAACAACGCAACAGCATCATATATCGATTGAGGGGACGG		1200
Qy	1201	GCTCAGTGA	AGTCTGGGACGACCAAGAGGTGACACGAGAGCTTCAAGAG		1260
Db	1201	GCTCAGTGA	AGTCTGGGACGACCAAGAGGTGACACGAGAGCTTCAAGAG		1260
Qy	1261	GGTCAGTGT	GTGTGGCCACAGAACTTCGCCGTGCTGGAAGTCCCAAGACGAGAAC		1320
Db	1261	GGTCAGTGT	GTGTGGCCACAGAACTTCGCCGTGCTGGAAGTCCCAAGACGAGAAC		1320

Qy	1321	TTCGAATAC	TGGCATTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAA		1380
Db	1321	TTCGAATAC	TGGCATTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAA		1380
Qy	1381	AACTCCGT	CATAGATAACCTGCGGAGGAGGTGTTGCAAAATTCATATGGCCTTCCAAAGG		1440
Db	1381	AACTCCGT	CATAGATAACCTGCGGAGGAGGTGTTGCAAAATTCATATGGCCTTCCAAAGG		1440
Qy	1441	GAGCAGGCA	AGGCGCTTAAGAAACAAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAG		1500
Db	1441	GAGCAGGCA	AGGCGCTTAAGAAACAAACCCCTTCAAGTTCTTCGTTCCACCGTCTCAG		1500
Qy	1501	CAGTCTCC	AGGCGCTTGGCTTAA		1524
Db	1501	CAGTCTCC	AGGCGCTTGGCTTAA		1524
RESULT 5					
AAS08540					
ID	AAS08540 standard; cDNA; 1524 BP.				
XX	AAS08540;				
XX	AC				
DT	23-OCT-2001 (first entry)				
XX	DNA encoding anaphylactic antigen Ara h 3.				
DE	Ara h 3; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;				
KW	allergy; mast cell; basophil; mouse; ss.				
KW	Mus sp.				
OS	Mus sp.				
XX	Mus sp.				
Key	Location/Qualifiers				
CDS	1..1533				
FT	/*tag= a				
FT	/product= "Peptide antigen Ara h 3"				
FT	/note= "Coding sequence of amino acids 1-3 not given"				
XX	WO200140264-A2.				
PN	07-JUN-2001.				
XX	06-DEC-2000; 2000WO-US033124.				
PF	06-DEC-1999; 99US-00455294.				
XX	23-JUN-2000; 2000US-0213765P.				
PR	27-SEP-2000; 2000US-0235797P.				
XX	(PANA-) PANACEA PHARM LLC.				
PA	(UYAR-) UNIV ARKANSAS				
PA	(MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.				
XX	Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;				
PI	WPI: 2001-381378/40.				
XX	P-PSDB; AAU04708.				
DR	Antigenic fragments useful for reducing anaphylactic risk and reducing				
PT	the severity and/or number of allergic symptoms in individuals sensitive				
PT	to antigens, have reduced ability to bind Immunoglobulin E.				
XX	Disclosure; Fig 11; 100pp; English.				
PS	The sequence represents the coding sequence of anaphylactic antigen Ara h				
XX	3. Ara h 3 is an anaphylactic antigen (A), which was used to design				
CC	antigenic peptides having a reduced ability to bind immunoglobulin E				
CC	(IgE) as compared with the intact (A), or having a sequence substantially				
CC	identical to a portion of sequence of an antigen that includes at least				
CC	one IgE binding site, where at least one IgE binding site of the peptide				
CC	is altered. The antigenic peptides are used in a composition which is				
CC	useful for reducing risk or severity of allergic reaction to an antigen.				
CC	This is done by identifying an individual at risk of allergic reaction to				

CC an antigen by identifying prior display of allergic symptoms when exposed
CC to the antigen, or a familial relationship with an individual who
CC previously displayed allergic symptoms when exposed to the antigen.
CC Following this an antigen-specific IgE present on one or more mast cells
CC or basophils in the individual's serum is identified. The individual is
CC then contacted with a peptide corresponding to a portion of the antigen,
CC which is selected, formulated, and delivered so that binding of the
CC peptide to antigen-specific IgE is reduced as compared with IgE binding
CC of intact antigen. The composition is also useful for treating and
CC preventing allergic reactions
XX
SQ Sequence 1524 BP; 455 A; 392 C; 396 G; 281 T; 0 U; 0 Other.

Query Match 99.8%; Score 1520.8; DB 4; Length 1524;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CGGCAGCAACCGGAGGAGAACGGGTGCCAGTTCACGGCCCTCAATGGCGAGACCTGAC	60
Db	1	CGGCAGCAACCGGAGGAGAACGGGTGCCAGTTCACGGCCCTCAATGGCGAGACCTGAC	60
Qy	61	AATCGCAATTGAATCAGAGGCGGTTACATTGAGACTTGGAAACCCCAACACACAGGAGTTC	120
Db	61	AATCGCAATTGAATCAGAGGCGGTTACATTGAGACTTGGAAACCCCAACACACAGGAGTTC	120
Qy	121	GAATGCGCCGCGGTGCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCCCTTCGTAGGCCT	180
Db	121	GAATGCGCCGCGGTGCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCCCTTCGTAGGCCT	180
Qy	181	TTCTACTCCAATGCTCCCAAGAGATCTTCATCAGCAAGGAAGGGGATCTTTGGGTTG	240
Db	181	TTCTACTCCAATGCTCCCAAGAGATCTTCATCAGCAAGGAAGGGGATCTTTGGGTTG	240
Qy	241	ATATTCCTGCTGCTCCTAGCACTATGAAGAGCTCACACAAAGTCTGCTCATCTCAG	300
Db	241	ATATTCCTGCTGCTCCTAGCACTATGAAGAGCTCACACAAAGTCTGCTCATCTCAG	300
Qy	301	TCCCAAGACCAACAGAGCTCTCCAGGAGAGAGACCAAGCCCAACAGCAACGAGATAGT	360
Db	301	TCCCAAGACCAACAGAGCTCTCCAGGAGAGAGACCAAGCCCAACAGCAACGAGATAGT	360
Qy	361	CACAGAGGTGACCGGTTTCGATGAGGGTGATCTCATCAGTTCACCGGTGTTGCT	420
Db	361	CACAGAGGTGACCGGTTTCGATGAGGGTGATCTCATCAGTTCACCGGTGTTGCT	420
Qy	421	TTCTGGCTCTACACGACACGACACTGATGTTGCTGCTTCTTACTGACACCAAC	480
Db	421	TTCTGGCTCTACACGACACGACACTGATGTTGCTGCTTCTTACTGACACCAAC	480
Qy	481	AACAAAGACCAACAGCTTGAATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACACGGAG	540
Db	481	AACAAAGACCAACAGCTTGAATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACACGGAG	540
Qy	541	CAAGAGTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGCAAGAGCTTACCATAT	600
Db	541	CAAGAGTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGCAAGAGCTTACCATAT	600
Qy	601	AGCCCATACAGCCGCAAGTACGCTTAGACAGAGAGCGTCAATTTAGCCCTCCGAGGA	660
Db	601	AGCCCATACAGCCGCAAGTACGCTTAGACAGAGAGCGTCAATTTAGCCCTCCGAGGA	660
Qy	661	CAGCAGACCGCCAGAGAACCGAGGAGCAAGAGAGAAACGAAGGTGGAACATCTTC	720
Db	661	CAGCAGACCGCCAGAGAACCGAGGAGCAAGAGAGAAACGAAGGTGGAACATCTTC	720
Qy	721	AGCGGCTTACCGCGGAGTTCCTGGAAACAAGCTTCAGGTTGACACAGACAGATAGTG	780
Db	721	AGCGGCTTACCGCGGAGTTCCTGGAAACAAGCTTCAGGTTGACACAGACAGATAGTG	780
Qy	781	CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGA	840
Db	781	CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGA	840

Qy	841	GGCTTCAGAAATCTTGAGCCAGATAGAAAGAGAGAGCTGCCGACGAAGAAGAGGAATACGAT	900
Db	841	GGCTTCAGAAATCTTGAGCCAGATAGAAAGAGAGAGCTGCCGACGAAGAAGAGGAATACGAT	900
Qy	901	GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGGTGGCAGGGAAGCAGAGGCGG	960
Db	901	GAAGATGAATATGAATACGATGAAGAGGATAGAAAGCGGTGGCAGGGAAGCAGAGGCGG	960
Qy	961	GGGAATGGTATTGAAGAGAGAGCTTCACCGCAAGTGTCTAAAAAGAACATTTGTTAGAAAC	1020
Db	961	GGGAATGGTATTGAAGAGAGAGCTTCACCGCAAGTGTCTAAAAAGAACATTTGTTAGAAAC	1020
Qy	1021	AGATCCCTGACATCTACAAACCTCAAGCTGTGTTCACTCAAACTGCCAACGATCTCAAC	1080
Db	1021	AGATCCCTGACATCTACAAACCTCAAGCTGTGTTCACTCAAACTGCCAACGATCTCAAC	1080
Qy	1081	CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCA	1140
Db	1081	CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCA	1140
Qy	1141	TTGTTTGTGCTCCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGACGG	1200
Db	1141	TTGTTTGTGCTCCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGACGG	1200
Qy	1201	GCTCAGCTGCAAGTCTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGTTCAGAG	1260
Db	1201	GCTCAGCTGCAAGTCTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGTTCAGAG	1260
Qy	1261	GGTCAAGTCTGCTGCTGACAGAACTTCGCGCTGCTGGAAAGTCCCAGAGCGAGAAC	1320
Db	1261	GGTCAAGTCTGCTGCTGACAGAACTTCGCGCTGCTGGAAAGTCCCAGAGCGAGAAC	1320
Qy	1321	TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCCGGTGAA	1380
Db	1321	TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCCGGTGAA	1380
Qy	1381	AATCCGTCTATAGATAAATCTCGCGAGAGGTGTTGCAAAATTCATATGGCCTCCAAAGG	1440
Db	1381	AATCCGTCTATAGATAAATCTCGCGAGAGGTGTTGCAAAATTCATATGGCCTCCAAAGG	1440
Qy	1441	GAGCAGGCAAGCAGCTTAAGAACAAACCCCTTCAAGTCTTCGTTCCACCGTCTCAG	1500
Db	1441	GAGCAGGCAAGCAGCTTAAGAACAAACCCCTTCAAGTCTTCGTTCCACCGTCTCAG	1500
Qy	1501	CAGTCTCCGAGGCTGTGGCTTAA 1524	
Db	1501	CAGTCTCCGAGGCTGTGGCTTAA 1524	

RESULT 6
AAF90338
ID AAF90338 standard; cDNA; 1855 BP.
XX AAF90338;
XX
XX 11-SEP-2003 (revised)
XX 23-JUL-2001 (first entry)
XX Peanut allergen Ara h4 cDNA.
XX Peanut; allergen; Ara h2; Ara h3; transgenic plant; allergy; ss.
XX Arachis hypogaea.
XX Key Location/Qualifiers
XX CDS 1..1593
XX FT /*tag= a
XX FT misc_feature 430..1190
XX FT /*tag= b
XX FT /note= "PCR amplified fragment"
XX XX WO200136621-A2.

PD 25-MAY-2001.
XX
PF 20-NOV-2000; 2000WO-US031657.
XX
PR 19-NOV-1999; 99US-0167255P.
XX
PA (UYAL-) UNIV ALABAMA A & M.
XX
PI Dodo HW, Arntzen CJ, Konan KN, Viquez OM;
XX WPI; 2001-355630/37.
XX
PT Producing transgenic peanut plants that produce allergen-free seeds,
XX useful in non-allergenic foods, by antisense or sense co-suppression of
XX allergen-encoding genes.
PS Claim 20; Fig 4; 72pp; English.
XX
CC The present sequence is that of peanut allergen Ara h3 cDNA. A portion of
CC the Ara h2 gene coding region is homologous to the corresponding region
CC of the peanut allergen Ara h4 gene. This region has been PCR amplified,
CC cloned in transformation vectors (pUC18 and pBI434) in sense and
CC antisense orientations and used to down-regulate Ara h3 and Ara h4
CC allergens in peanut. This is an example of the method of the invention,
CC which relates to the production of a peanut plant having reduced, or
CC undetectable, allergenic protein (AP) content in its seed. A peanut plant
CC cell is transformed with a DNA construct containing an antisense AP gene
CC and/or sense AP gene, or their fragments, regenerated to plants, and
CC fertile transgenic plants that produce seeds with reduced AP content are
CC identified. The seeds are useful for preparation of allergen-free foods.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 1855 BP; 564 A; 430 C; 465 G; 396 T; 0 U; 0 Other;

Query Match 91.3%; Score 1391.2; DB 4; Length 1855;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 68; Indels 2; Gaps 2;

QY 2 GGAGCAACCGGAGGAGAACCGGTGCGAGTTCAGGCGCTCAATGCGCAGAGACCTGACA 61
DB 71 GGAGCAGCGCGGAGGAGATGCGTGGCAGTTCAGGCGCTCAATGCGCAGAGACCTGACA 130
QY 62 ATCGCATTTGAATCAGAGGGCGGTACATTCAGACTTTGGAAACCCCAACACAGGAGTTCG 121
DB 131 ACCGCATTGAATCGGAGGGCGGTACATTCAGACTTTGGAAACCCCAACACAGGAGTTCG 190
QY 122 AATGCGCGCGCGTGGCCCTCTCTCGTTAGTCTCCGCGCAACGCCCTTCGTAAGCCTT 181
DB 191 AATGCGCGCGCGTGGCCCTCTCTCGTTAGTCTCCGCGCAACGCCCTTCGTAAGCCTT 250
QY 182 TCTACTCCAAATGCTCCCGAGGAGATCTTCATTCAGCAGAGGAGGAGTACTTTGGGTGA 241
DB 251 TCTACTCCAAATGCTCCCGAGGAGATCTTCATTCAGCAGAGGAGGAGTACTTTGGGTGA 310
QY 242 TATTTCCCTGCTGTCTCTAGACACTATGAGAGGCTTCACACAAAGGTCTCGATCTCAGT 301
DB 311 TATTTCCCTGCTGTCTCTAGACACTATGAGAGGCTTCACACAAAGGAGGAGTATCAGT 370
QY 302 CCCAAAGACCAACCAAGACGCTCTCCAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTC 361
DB 371 CCCAAAGACCAACCAAGACGCTTTCAGAGAGAGAACCAAGCCCAACAGCAACAGATAGTC 430
QY 362 ACAGAGAGGTGCACCGTTTCGATGAGGGTGCATCTCATTGAGTTCACCGCGGTGTCCTT 421
DB 431 ACCAGAGAGGTGCACCGTTTCGATGAGGGTGCATCTCATTGAGTTCACCGCGGTGTCCTT 490
QY 422 TCTGGCTCTCAACGACACGACACTGATGTGTGTGCTGTTCTCTTACTGACACCAACA 481
DB 491 TCTGGCTGTCAACGACACGACACTGATGTGTGTGCTGTTCTCTTACTGACACCAACA 550
QY 482 ACAACGACCAACGAGTTCAGTTCCTCCAGGAGATTCATTTGGCTGGGAAACAGCGAGC 541
DB 551 ACAACGACCAACGAGTTCAGTTCCTCCAGGAGATTCATTTGGCTGGGAAACAGCGAGC 610

QY 542 AAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAGAGAGCTTACCATATA 601
DB 611 AAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAGAGAGCTTACCATATA 670
QY 602 GCCCATACAGCCCGCAAAGTTCAGCCCTTAGACAAGAAGAGCGTGAATTTAGCCCTTCGAGGAC 661
DB 671 GCCCATACAGCCCGCATAGTTCGCTTAGACGAGAGAGCGTGAATTTCCGCTTCGAGGAC 730
QY 662 AGCACAGCCGACAGAGAACGAGCAGGACAAAGAAAGAAACCAAGGTGGAACATCTTCA 721
DB 731 AGCACAGCCGACAGAGAACGAGCAGGACAAAGAAAGAAACCAAGGTGGAACATCTTCA 790
QY 722 GGGCTTCACGCGGAGTTCCTGGACAGCCTTCAGGTTCCAGGTTCCAGCAGACAGATAGTC 781
DB 791 GCGGCTTCACGCGGAGTTCCTGGACAAAGCCTTCAGGTTCCAGCAGACAGATAGTC 850
QY 782 AAAACCTAAGAGCGCAGACCGGAGAGTGAAGAAGAGGAGCCATTTGTGACAGTGAGGGAG 841
DB 851 AAAATCTGTGGGCGGAGAACGAGAGTGAAGAAGAGGAGGCCATTTGTGCGGTGAGGGAG 910
QY 842 GCTCAGAATCTTTAGGCCCCAGATAGAAAGAGACGTGCCCGACGAGAGGAATACGATG 901
DB 911 GCTCAGAATCTTTAGGCCCCAGATAGAAAGAGAGGTGCCCGACGAGAGGAATACGATG 970
QY 902 AAGATGAATATGAATACGATAGAGGATAGAGGCGTGGCAGGGGAAACGAGAGGACGG 961
DB 971 AAGATCAATATGAATACCAATGAGAGGTGAAGGCGTGGCAGGGGAAACGAGAGGCGGG 1030
QY 962 GGAATGGTATTGAAGAGACGATCTGCACGCGCAAGTCTAAAAAGAACATTTGTGAGAAACA 1021
DB 1031 GGAATGGTATTGAAGAGACGATCTGCACGCGCATGCTTAAAAAGAACATTTGTGAGAAACA 1090
QY 1022 GATCCCTGACATCTAACACCTCA--AGCTGGTTCACTAAAACTGCCAACGATCTCAAC 1080
DB 1091 GATCCCTGACATCTAACGATCTCTCAGCGTGGTTCACTCAAACTGCC--ACGATCTCAAC 1149
QY 1081 CTTCTAATCTTAGGTGGCTTGACCTAGTCTGTAATATGGAAATCTCTACAGGAATGCA 1140
DB 1150 CTTCTAATCTTAGGTGGCTTGACCTAGTCTGTAATATGGAAATCTCTACAGGAATGCA 1209
QY 1141 TTGTTTGTGCTCAGTCAACACCAACGACACAGCATCATATATCGATTGAGGGGACGG 1200
DB 1210 TTGTTTGTGCTCAGTCAACACCAACGACACAGCATCATATATCGATTGAGGGGACGG 1269
QY 1201 GCTCAGTGCAGTCTGTGACAGCAACGCGCAACAGAGTGTACGACGAGGCTTCAAGAG 1260
DB 1270 GCTCAGTGCAGTGTGTGACAGCAACGCGCAACAGAGTGTACGACGAGGCTTCAAGAG 1329
QY 1261 GGTACGTCCTTGTGTGTCACAGAACTTCGCGCTGCTGGAAAGTCCACAGAGCGAGAAC 1320
DB 1330 GGTACGTCCTTGTGTGTCACAGAACTTCGCGCTGCTGGGAGTCCACAGAGCGAGAAC 1389
QY 1321 TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACTTCGCGGTGAA 1380
DB 1390 TTGGAATACGTGGCATTCAAGACAGACTCAAGGCCCAGCATAGCCAACTTCGCGGTGAA 1449
QY 1381 AACTCGTCATAGATAACCTCGCGGAGGAGGTGGTTGCAAAATTCATATGCGCTCCAAAGG 1440
DB 1450 AACTCGTCATAGATAACCTCGCGGAGGAGGTGGTTGCAAAATTCATATGCGCTCCAAAGG 1509
QY 1441 GAGCAGGCAAGGAGGCTTAAGAAACAAACCCCTTCAAGTTCCTCGTTCCACGCTCTCAG 1500
DB 1510 GAGCAGGCAAGGAGGCTTAAGAAACAAACCCCTTCAAGTTCCTCGTTCCACGCTCTCAG 1569
QY 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524
DB 1570 CAGTCTCCGAGGCTGTGGCTTAA 1593

RESULT 7
AAV17567
ID AAV17567 standard; cDNA; 1446 BP.

[illegible]

Db	1247	AGTATGTTTCATTCAAGACCAATGATAGACCTCGATCGGCAACCTTGCAGGTGCAAACT	1306
Qy	1385	CCGTCATAGATAACCTCCGGAGGAGGTGGTTGCAAAATTCATATGGGCTCCAAAGGAGC	1444
Db	1307	CATTGTTGACGATTCGCGGAGGAAGTGATTACAGAAACTTTTAACCTAAGGAGGAGC	1366
Qy	1445	AGGCAAGGAGCTTAAAGAACAAACCCCTTCAAGTTCCTGGTTCCACCGTCTCAGCAGT	1504
Db	1367	AGGCCAGGAGGTCAAGAACAAACCCCTTTCAGCTTCCTGGTTCCACCTAAGGAGTCTC	1426
Qy	1505	CTCGAGGGCTGTGGCTTA	1523
Db	1427	AGAGGAGAGTTGTGGCTTA	1445
RESULT 8			
ABS55193			
ID	ABS55193 standard; DNA; 1446 BP.		
XX			
AC	ABS55193;		
XX			
DT	17-DEC-2002 (first entry)		
XX			
DE	Glycine max (Soybean) var. Dare gene.		
XX			
KW	Soybean; Glycinin; atomic coordinate data; processability; soya protein;		
KW	Dare; protein co-ordinate data; gene; ds.		
XX			
OS	Glycine max.		
XX			
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
FT	1..1446		
FT	/*tag= a		
FT	/product= "Glycine max (Soybean) var. Dare protein"		
XX			
PN	JP2002193996-A.		
XX			
PD	10-JUL-2002.		
XX			
PF	21-DEC-2000; 2000JP-00405097.		
XX			
PR	21-DEC-2000; 2000JP-00405097.		
XX			
PA	(KYOU) UNIV KYOTO.		
XX			
DR	WPI; 2002-685438/74.		
DR	P-PSDB; ABG71266.		
XX			
PT	Glycinin, beta-conglycinin and proglycinin, their crystal structures,		
PT	three dimensional coordinates, three dimensional structured and models		
PT	and their uses.		
XX			
PS	Disclosure; Page 1271-1273; 1298pp; Japanese.		
XX			
CC	The present invention relates to a new Glycinin characterised by the		
CC	atomic coordinate data fully defined in the specification. The structure		
CC	can be used for improving processability of soya protein. The present		
CC	nucleic acid sequence encodes the Glycine max (Soybean) var. Dare		
CC	protein, as described in the specification		
XX			
SQ	Sequence 1446 BP; 426 A; 361 C; 354 G; 305 T; 0 U; 0 Other;		
Query Match 34.0%; Score 517.4; DB 6; Length 1446;			
Best Local Similarity 62.8%; Pred. No. 1.7e-137;			
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;			
Qy	5	AGCAACGGAGGAGAACCGCTGCCAGTTCAGCGCCTCAATGCCAGAGACCTGACAATC	64
Db	71	AGCAGGCACAGCAAAACGAGTGCAGATCCAAAGCTCAATGCCCTTAAACCCGGATAACC	130
Qy	65	GCATTGAATCAGAGGGCGGTTTACATTGAGACTTTGGAACCCCAACACCGAGGTTTCAAT	124

Db	131	GTATAGATCAGAAAGTGGCTTCATTGAGACATGGNACCCTAACAAACAGCCATTCAGT	190
QY	125	GGCGCGCGCTCCGCTCTCTCGCTTAGTCTCTCGCGGCAACGCCCTTCGTAGGCTTTCT	184
Db	191	GTGCGCGTGTGGCTCTCTCGCTGACCTCAACCGCAACGCCCTTCGACAGACCTTCCT	250
QY	185	ACTCCNATGCTCCGAGGAGATCTTCACGACNAGGAGGGGATACTTTGGTTGATAT	244
Db	251	ACACCAAGCTCCGAGGAGATCTACATCCAAAGGTAGTGGTATTTTGGCATGATAT	310
QY	245	TCCCTGTTGTCTTAGACACTATGAAGAGCCTCACACAAAGTCTCGATCTCAGTCCC	304
Db	311	TCCGCGTGTCTTAGCACATTTGAAGGCT-----	342
QY	305	AAAGACCAAGACGCTCTCAAGGAGAAAGCAAAAGCCAAACAGCAACGAGATAGTCACC	364
Db	343	-----CAACAAAAAGGACAAAGCAGCAGGCGCCCAAGACCGTCACC	382
QY	365	AGAAGTGCACCGTTTCGATGAGGTTGATCTCATTTGCAGTTCCTCCACCGGTGTTCTTCT	424
Db	383	AGAAGATCTATCATTTCAGAGAGGGTGATTTGATTGCAGTGCACCGGTTTTCATCT	442
QY	425	GGCTCTACAAACGACCAACGACACTGATGTTGTTGCTGTTTCTCTTACTGACCAACAACA	484
Db	443	GGATGTACAACAATGAAGACACTCTCTGTTGTTGCGGTTTCTCTTATTGACACCAACAGCT	502
QY	485	AGCAACACAGCTTGATTCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACAACGAGCAAG	544
Db	503	TCAGAAACAGCTCGACCAAGATGCTTAGGAGATTCTATCTGCTGGGAACCAAGAGCAAG	562
QY	545	AGTTCTTAAGTTACCAGCAACAAAGCAGACAAAGCAGACAGCAAGAAAGCTTTACCATATAGCC	604
Db	563	AGTTTCTCAGTATCAGCCACAGAAAGCAGCAAG-----	595
QY	605	CATACAGCCGCAAAAGTTCAGCCTTAGACAAAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC	664
Db	596	-----GAGGTACTC	604
QY	665	ACAGCCGAGAGAAACGAGCAGGACAAAGAAAGAAAGAAACGAGGTGGAACATCTTCAGCG	724
Db	605	AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAAGAAACGAGGAGGACGATATTGAGTG	664
QY	725	GCTTCACGCGGAGTTCTTGGAACCAAGCTTCCAGGTTGACGACACAGATAGTCAAA	784
Db	665	GCTTCGCCCGGAATCTTGGAAACATGCGTTC---GTCGTGCACAGCAGATAGTGAGAA	721
QY	785	ACCTAAGAGCGCAGACCGAGAGTGAAGAGAGGGAGCCATTGTGACAGTGAAGGGAGGCC	844
Db	722	AGCTACAAGGTGAGAAACGAAAGAGGAGAAAGGGTGCCATTGTGACAGTGAAGGAGGTC	781
QY	845	TCAGATCTTGAGCCGAGATAGAAAGAGACGTGCCGACGAGAGAGGAATACGATGAAG	904
Db	782	TCAGCGTGATAAGCCCAACCGGAGAGCAGCAACAAAGACCCGAGGAGAGGAGAGC	841
QY	905	ATGAATATCAATACGATGAAGAGGATAGAAGGCGTGGCAGGGGAGAACAGAGGAGGAGGGA	964
Db	842	CAGATTGTGACGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA	886
QY	965	ATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTAAAAAGAACATTTGGTAGAAACAGAT	1024
Db	887	ATGGCATTGACGAGACCAATTTGCACAAATGAGACTTCGCCACACAAATTTGGCAGACTTCAT	946
QY	1025	CCCTTGACATCTACACCTCAAGCTGAGTTCCTCAAACTGCCAAGATCTCAACCTTC	1084
Db	947	CACCTGACATCTCAACCTCAAGCTGGTAGCATCAACCGCTACAGCCTCGACTTC	1006
QY	1085	TAATACCTTAGGTGGCTTTGGACCTTAGTGTGTAATATGGAATCTCTACAGGAATTCATTTGT	1144
Db	1007	CAGCCCTCTCTGGCTCAAACTCAGTGCCTCAGTTTGGATCACTCCCGAAGATTCATGT	1066
QY	1145	TTGTGCTCTACTACAAACACGACAGCATCATATATCGATTGAGGGGAGCGGCTC	1204
Db	1067	TCGTGCCACACTACAACTGAACGCAACAGCATATAATACGCAATTTGAATGGAGCGGCAT	1126

185 ACTCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATCTTTGGGTGATAT 244
186 |||||
187 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGGTATTTTGGCATGATAT 310
188 |||||
189 TCCTGTGCTTCCTAGACATATGAAGGCTTCACACAAAGGTGCTGATCTCAGTCCC 304
190 |||||
191 TCCCGGTGTGCTTAGCACATTTGAAGGCT----- 342
192 |||||
193 AAAGACCAACCAAGACGCTCTCCAGGAGAAACCAAGCCAAACAGACGAGATAGTCACC 364
194 |||||
195 -----CAACAAAGGACAAAGCAGCAGGCCCAAGACCGTCACC 382
196 |||||
197 AGAAGTGCAACCGTTTCGATGAGGGTGAATCTATTGCAAGTTCCACCGGTGTTGCTTCT 424
198 |||||
199 AGAAGATCTATCACTTCAGAGAGGGTGAATTTGATTGCAAGTCCCAACCGGTTTGCATAT 442
200 |||||
201 GGCTCTACACGACCAACGACATGATCTGTTGCTGTTTCTCTACTGACACCAACAA 484
202 |||||
203 GGATGTACAAATGAAGACACTCCTGTTGTCGGTTTCTCTATTGACACCAACAGCT 502
204 |||||
205 ACAGCAACACGAGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACACGAGCAAG 544
206 |||||
207 TCCAGAACACGCTCGACAGATGCTAGGAGATCTATCTTGTGCTGGGAACAGAGCAAG 562
208 |||||
209 AGTTCTTAAGGTACCAACAAACAAAGCAGACAAAGCAGCAAGAGCTTACCATATAGCC 604
210 |||||
211 AGTTCTACAGTATCAGCCACAGAGCAGCAAG----- 595
212 |||||
213 CATACAGCCGCAAGTTCAGCTAGACAGAGAGCGTGAATTTAGCCCTCGAGGACAGC 664
214 |||||
215 -----GAGGTACTC 604
216 |||||
217 ACAGCCGACAGACGAGCAGGACAAAGAAACGAAAGGTGGAAACATCTTTCAGCG 724
218 |||||
219 AAGCCAGAAAGGAAACGCTCAGCAGAAAGAAACGAGGAGGAGCATATTGAGTG 664
220 |||||
221 GCTTACGCGCGAGTTCTCTGGAACAAACCTTCCAGGTTGACGACAGACATAGTCAAA 784
222 |||||
223 GCTTCGCGCGGAATCTTGGAAATCGCTTC---GTGCTGGACAGGACAGATAGTAGAA 721
224 |||||
225 ACCTAGAGGCGAGCAGCAGGATGAGAAAGAGGAGGAGGATTTGACAGTGAAGGGAGGCC 844
226 |||||
227 AGCTAAGGTGAGAACGAGAGGAAGAGAGGAGGTCATTTGACAGTGAAGAGGAGGTC 781
228 |||||
229 TCAGAAATCTTTGAGCCAGATAGAAAGAGAGCTGCTCCAGCAAGAGAGGAAATACGATCAAG 904
230 |||||
231 TCAGCGTGATAAGCCACCCACCGAGAGCAGCAACAAAGACCCGAGAGAGAGAGC 841
232 |||||
233 ATGAATATGAATACGATGAAGAGGATAGAAAGGCTGGCAGGGGAAGCAGAGGAGGGGA 964
234 |||||
235 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA 886
236 |||||
237 ATGGTATTGAAGAGACGATCTGACCCGCAAGTGTAAAGAAACATTTGGTAGAAACAGAT 1024
238 |||||
239 ATGGCATTTGACGAGACCAATTTGACAAATGAGACTTCCGCAACATTTGGCCAGACTTCAT 946
240 |||||
241 CCCTGACATCTCAACCCCTCAAGCTGGTTCACTCAAAAGTGCACACGATCTCAACCTTC 1084
242 |||||
243 CACTGACATCTTCAACCCCTCAGCTGAGTGTAGATCAACACCGCTACCGCTCGACTTC 1006
244 |||||
245 TAATACTAGGTGGCTTGGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCAATTGT 1144
246 |||||
247 CAGCCCTCTCTGCTCAAACTCAGTGCCTCAGTTGGATCACTCCGCAAGAAATGCTATGT 1066
248 |||||
249 TTGTCGCTCACTCAACCAACGACACGACATCATATATATGATTTGAGGGGAGGGGCTC 1204
250 |||||
251 TCGTGCCACACTCAACCTCAAGCGCAACGACATATATACGATTTGAATGTCAGGCGCAT 1126
252 |||||
253 ACGTGAAGTCTGTGGAAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264
254 |||||
255 TGGTACAAAGTGGTGAATTTGCAATGGTGAGAGAGTGTGTTGATGAGAGCTCCAGAGGGAC 1186
256 |||||
257 ACGTGTCTGTGGTGCCACAGAACTTTCGCGCTCGTGGAAAGTCCACAGAGCAGAACTTCG 1324

1187 AGGTGTTAAATGTGCCACAAAACCTTTGCGGTGGCTGCAAGATCACAGAGCGCAACTTCG 1246
1188 |||||
1325 AATACGTGGCATTTCAAGACAGACTCAAGGCCAGCATAGCAACCTCGCGGTGAAGACT 1384
1326 |||||
1247 AGTATGTTTTCATTCAAGACCAATGATAGACCCCTCGATCGGCAACCTTGCAGGTGCAAACT 1306
1327 |||||
1385 CCCTCATAGATAACCTCGCGGAGGAGTGGTTGCAAAATTCATATGGCTTCCAAAGGGAGC 1444
1386 |||||
1307 CATTGTTGAACGATTGCGCGAGGAAGTGAATTCAGCAAACTTTTAACCTAAGGAGGAGC 1366
1387 |||||
1445 AGCAAGGAGCTTAAGAAACAAACCCCTTCAAGTTCTTGGTTCACCGTCTCAGCAGT 1504
1388 |||||
1367 AGCCAGGAGGTCAGAAACAAACCCCTTTCAGCTTCTGTTCCACCTTAAGGAGTCTC 1426
1389 |||||
1505 CTCGAGGCGTGGGCTTA 1523
1390 |||||
1427 AGAGGAGATTGTGGCTTA 1445
1391 |||||
RESULT 11
ADX12705
ID ADX12705 standard; cDNA; 1673 BP.
XX
XX ADX12705;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 7280.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIU/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TAB/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 7280; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. the polynucleotide
XX of the invention are also useful in physical arrays of molecules and as

CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomanan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1673 BP; 501 A; 402 C; 396 G; 374 T; 0 U; 0 Other;
Query Match 34.0%; Score 517.4; DB 13; Length 1673;
Best Local Similarity 62.8%; Pred. No. 1.8e-137;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;
QY 5 AGCAACCGGAGGAGAACGGCTGCCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC 64
DB 93 AGCAGCCACAGCAAAACGAGTGCAGATCCAACGCCTCAATGCGCTCAAAACCGGATAACC 152
QY 65 GCATTGAATCAGAGGGGGTTAATTGAGACTTTGGAAACCCACCAACACAGGAGTTGCAAT 124
DB 153 GTATAGAGTCAGAGGTGGGTTTCAATTGAGACATGGAAACCCATAACAAGCCATTCCAGT 212
QY 125 GCGCCGGCGTCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCCCTTCT 184
DB 213 GTGCCGGTGTGCCCTCTCTCGCTGACCCCTCAACCGCAACGCCCTTCGACAGACCTTCT 272
QY 185 ACTCCAAATGCTCCCGAGGAGATCTTCATCCAGCAAGAAAGGGATATCTTTGGTTGATAT 244
DB 273 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGTATTTTGGCATGATAT 332
QY 245 TCCCTGGTTGCTAGACATATGAAGAGCCTCACACAGAGTCTCGTCTGATCTCAGTCCC 304
DB 333 TCCCGGGTTGCTTAGCACATTTGAAGAGCCT----- 364
QY 305 AAAGACCAACAGACGCTCTCAAGGAGAGAACCAAGCCAAACAGCAACGAGATGATCACC 364
DB 365 -----CAACAAAGGACAAAGCAGCAGCGCCCAAGACCGTCAAC 404
QY 365 AGAAGTGACACCGTTTCGATGAGGGTGAATCTATTGCAAGTTCCTCCACCGGTGTTGCTTCT 424
DB 405 AGAAGATCTATCACTTCAGAGAGGGTGATTTGATGTCAGTGCACACCGGTTTTCATCT 464
QY 425 GGCTCTACACGACCCAGCAGACTGATGTTGCTGTTTCTCTTACTGACACCAACAACA 484
DB 465 GGATGTACAAATGAAGACACTCCTGTTGTTGCCGTTTCTCTATTTGACCAACACAGCT 524
QY 485 ACACCAACACAGCTTGATCACTTCCCGAGGAGATTCAATTTGGCTGGGAACACCGGCAAG 544
DB 525 TCCAGAACACAGCTCGACCATGCTTAGGAGATTCTATCTTCTGGGAACCAAGAGCAAG 584
QY 545 AGTTCTTAAGGTACCGACAAACAAAGCAGACAAGAGCAGACGAAAGCTTACCATATAGCC 604
DB 585 AGTTTCTACAGTATCAGCCACAGAACGACGCAAG----- 617
QY 605 CATACAGCCCGCAAGTCACTACGCTTAGACAAGAGCGTGAAATTTAGCCCTTCGAGGACAGC 664
DB 618 -----GAGGTACTC 626
QY 665 ACAGCCGACAGAACGACGAGGACAAGAGAAGAAAACGAAGGTGGAAAACATCTTCAGCG 724
DB 627 AAAGCCAGAAAGGAAAGCGTCAACAGAAAGAAACGAAGGAGGAGGAGCATATTAGTG 686
QY 725 GCTTCAGCCCGGAGTTCTCTGGAAACAAAGCCTTCAGGTTGACGACAGATAGTCAAA 784
DB 687 GCTTCGCCCGGAAATCTTGGAAACATCGGTTTC---GTCGTGGACAGGACATAGTGAGAA 743
QY 785 ACCTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGGGGAGGCC 844

DB 744 AGCTCAAGGTGAGAAACGAAGAGAAAGGGTGCCATTGTGACAGTGAAGAGGAGTC 803
QY 845 TCAGAAATCTTTAGCCCCAGATAGAAAGAGACGTGCCCGACGAAGAGAGGAATACGATGAAG 904
DB 804 TCAGCGTGATAGCCCCACCCACCGAAGACGACGCAACAAGACCCCGAGGAAGAGAGAGC 863
QY 905 ATGAATATGAATACGATAGAGAGGATAGAAAGCGGTGGCAGGGGAAGCAGAGGAGGGGA 964
DB 864 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCCAAAGCAGAA 908
QY 965 ATGGTATTCAAGAGACGATCTGCACCGCAAGTGCTAAATAAAGAACATTTGTTAGAAAACAGAT 1024
DB 909 ATGGCAATTCAGGAGACCATTTGCACAATGAGACTTCGCCACAACATTTGCCAGACTTCAT 968
QY 1025 CCCCTGACATCTACAAACCCCTCAAGCTGGTTCACTCAAAATCTGCCAACGATCTCAACCTTC 1084
DB 969 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACAACCGCTACCAGCTCGACTTCC 1028
QY 1085 TAATACCTTAGTGGCTTGGACCTAGTCTGATATATGGAATCTCTACAGAAATGCAATTGT 1144
DB 1029 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCAGTTTGGATCACTCCGCAAGAATGCTATGT 1088
QY 1145 TTGTCTCTCACTACAAACACCAACGCAACAGCATCATATATCGATTGAGGGGACGGGCTC 1204
DB 1089 TGTGCCACACTACAACCTGAAACGCAACAGCATATATATACGATTTGAATGGACGGGCAT 1148
QY 1205 AGTGCAAGTCTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264
DB 1149 TGTCAAGTGGTGAATTCGAATGGTGGAGAGTGTGATGGAGAGCTGCAAGAGGGAC 1208
QY 1265 AGTGCTTGTGGTCCACAGAACTTCGCGTGGTGAAGTCCGAGAGGAGGAGAACTTCG 1324
DB 1209 AGTGTTAATTTGTGCCACAAACTTTTGGCTGGCTGCAAGATCAGAGAGCGCAACTTCG 1268
QY 1325 AATACGTGCACTTCAAGACAGACTCAAGGCCAGCATAGCAACCTCGCGGTGAAAACT 1384
DB 1269 AGTATGTTTCAATTCAGACCAATGATAGACCTCGATCGGCAACCTTGCAGGTGCAACT 1328
QY 1385 CGGTCAATAGATAAACCCTCGGAGGAGGTGGTTGCAAAATTCATATGCGCTCCAAAGGAGC 1444
DB 1329 CATTTGTTAAACGATTTGCCGAGGAAGTGAATTCAGCAAACTTTTAACTTAAGAGGAGCAGC 1388
QY 1445 AGCAGGCGAGCTTAGAACAACACCCCTTCAAGTTCTTCTGTTCCACCGTCTCAGCAGT 1504
DB 1389 AGGCCAGGCGAGGTCAAGAAACAACCCCTTTCAGCTTCTCTGGTTCCACCTTAAGAGGAGTCTC 1448
QY 1505 CTCGAGGGGCTGTGGCTTA 1523
DB 1449 AGAGGAGAGTTGTGGCTTA 1467
RESULT 12
ADX13956
ID ADX13956 standard; cDNA; 1689 BP.
XX
AC ADX13956;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 8531.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX

PN US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 8531; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photoynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 1689 BP; 504 A; 408 C; 396 G; 381 T; 0 U; 0 Other;
SQ
Query Match 34.0%; Score 517.4; DB 13; Length 1689;
Best Local Similarity 62.8%; Pred. No. 1.8e-137;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;
QY 5 AGCAACGGAGGAGAACCGCTGCAGTTCAGCGCCTCAATGCCAGAGACCTGACATC 64
DB 105 AGCAGGCACAGCAAAACAGTGGCAGATCCAAACGCTCAATGCCCTCAAAACCGGATAACC 164
QY 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTTGGAAACCCCAACACAGAGGTTGCAAT 124
DB 165 GTATAGNGTCAGAAGGTGGCTTCATTGAGACATGGAAACCCCTAACACAGCCATTCCAGT 224
QY 125 GCGCCGGCGTGGCCCTCTCGTCTAGTCTCGCCGCGCAACAGCCCTTCGAGGCCCTTCT 184
DB 225 GTGCGGGTGTGGCTCTCTCGTCTGACCCCTCAACCGCAACGCCCTTCGAGACCTTCCT 284
QY 185 ACTCCAAATGCTCCCGAGGATCTTCATCCAGCAAGAGGGGATACCTTTGGTGTATAT 244
DB 285 ACACCAACGCTCCCGAGGAGATCTACATCCCAACAGGTAGTGTATTTTGGCATGATAT 344
QY 245 TCCCTGTGTCTCTAGACACTATGTAAGAGGCTCACACACAGGTCTCGTCTCAGTCCC 304
DB 345 TCCCGGGTGTCTCTAGACACTTTGAAAGGCTT----- 376
QY 305 AAAGACCACCAAGACGCTCTCCAGGAGAGAGACCAAGCCNAAGCAACGAGATAGTCACC 364

377 -----CAACAAAAAGGACAAAGCAGAGCGCCCAAGAGCGTCAAC 416
365 AGAAGGTGCAACCGTTTCGATGAGGGTGATCTCAATTCAGTTCCTCCACCGGTGTTGCTTCT 424
417 AGAAGATCTATCACTTCAGAGAGGGGTGATTTGATTCAGTTCGCAACCGGTTTGCATACT 476
425 GGCTCTACAACAGCACGACACATGTTGTTGCTGTTCTCTTACTGACACCAACAACA 484
477 GGATGTACAACAATGAAGACACTCTCTGTTGCTGCGTTCTTTATTTGACACCAACAGCT 536
485 ACACAAACAGCTTGTATCAGTTCCTCCAGAGGATTTCAATTTGGCTGGGAAACAGGAGCAAG 544
537 TCCAGAAACAGCTTCGACCAATGCTAGGAGATTTCTATCTTGTCTGGGAAACCAAGAGCAAG 596
545 AGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACAAAGAGCTTACCATATAGCC 604
597 AGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACAAAGCAGACAAAGCAGACAAAG 629
605 CATACAGCCCGCAAGTTCAGCTTAGACAAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
630 -----GAGGTACTC 638
665 ACAGCCGAGAGAAACGAGCAGGACAAGAAAGAAACGAAAGGTGAAACATCTTCAGCG 724
639 AAAGCCGAGAAAGGAAAGCGTTCAGCAAGAAAGAAAGGAGGAGGAGGAGGAGGAGGAGG 698
725 GCTTACGCGCGGAGTTCTTGGAACAGCTTCCAGGTTCAGCAGACACAGATAGTCAAA 784
699 GCTTCCGCCCGGAAATTTCTTGGAACATGCGTTC-----GTCTGGACAGGAGATAGTGAA 755
785 ACCTAAGAGGCGAGACGAGAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 844
756 AGCTACAAGTTCAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 815
845 TCAGAAATCTTGAGCCCGAGATAGAAAGAGAGCTGCCAGCAAGAAAGAGGAGGAGGAGGAG 904
816 TCAGCGGTGATTAAGCCCAACGAGAGAGCAGCAACAAAGAGGAGGAGGAGGAGGAGGAGG 875
905 ATGAATATCAATACATGAGAGGATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 964
876 CAGATTGTGACGAGAAAGACAACAT-----TCCAAAGCCCAAGCAGAA 920
965 ATGGTATTGAAGAGAGATCTGCACCGCAAGTCTAAAAAGAAACATTGGTAGAAACAGAT 1024
921 ATGGCATTGACGAGACCAATTGCAATGAGACTTCGCCACACATTTGGCCAGACTTTCAT 980
1025 CCCTGACATCTACAAACCTCAAGCTGGTTTCACTCAAAACCTGCAAGGATCTCAACCTTC 1084
981 CACCTGACATCTTCAACCTCAAGCTGGTAGCATCAACCCGCTACAGCTTCGAGCTTCC 1040
1085 TAATAGTCTAGGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATGCTATTGT 1144
1041 CAGCCCTCTGTGGCTTCAAACTCAGTGGCCAGTTTGGATCTCTCGCAAGATGCTATGT 1100
1145 TTGTGCTCTCACTACAAACCAACGCAACAGCATATATATCGATTGAGGGGAGCGGCTC 1204
1101 TGTGCGCACACTACAAACCTGAAACGCAACAGCATATATATACGATTGATGGACGGCAT 1160
1205 AGTGAAGTCTGGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264
1161 TGGTA CAAGTGGTGAATTGCAATGGTGGAGAGTGTGTTGATGGAGAGCTGCAAGAGGGAC 1220
1265 AGTGTCTTGTGGTCCACAGAACTTCGCGTCTGCGTGAAGTCCAGAGCGAGAACTTCG 1324
1221 AGTGTGTTAATTTGCGCAAAACCTTTCCGCTGGCTGCAAGATCACAGAGGAGCACTTCG 1280
1325 AATACGTGGCATTTCAAGACAGACTCAAGGCCCGCAGCATAGCAACCTTCGCGGTGAAACT 1384
1281 AGTATGTTTCAATTCAGAGCAATGATAGACCTTCGATCGCAACCTTCGAGGTGCAACT 1340
1385 CGGTCAATAGATAACCTTCGCGGAGGAGGTGGTTGCAAAATTCATATGCGCTTCCAAAGGAGC 1444

Db 1341 CATTGTTGAACGATTGCCGGAGGAAGTGAATTCAGCAAACTTTTAACCTAAGGAGCAGC 1400
Qy 1445 AGCAAGGCGAGCTTAAGAACAAACCCCTTCAAGTTCCTTCACCGTCTTCAGCAGT 1504
Db 1401 AGGCCAGGCGAGTCAAGAACAAACCCCTTTCAGCTTCCTGGTTCCACCTAAGGAGTCTC 1460
Qy 1505 CTCGAGGCGTGGGCTTA 1523
Db 1461 AGAGGAGAGTTGTGGCTTA 1479
RESULT 13
ADK14017
ID ADK14017 standard; cDNA; 1694 BP.
XX
AC
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 8592.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 8592; 15pp; English.
PS
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?docid:2004034888. the polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one

CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1694 BP; 504 A; 410 C; 397 G; 383 T; 0 U; 0 Other;
Query Match 34.0%; Score 517.4; DB 13; Length 1694;
Best Local Similarity 62.8%; Pred. No. 1.8e-137; Indels 144; Gaps 4;
Matches 954; Conservative 0; Mismatches 421;
Qy 5 AGCAACCGGAGGAGAACGGTCCAGTTCAGCGCTCAATGCGCAGAGACCTTGACAATC 64
Db 103 AGCAGCCACAGCAAAACGAGTGCCAGATCCAGCGCTCAATGCCCTCAAAACCGGATAACC 162
Qy 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACACAGGAGTTGCAAT 124
Db 163 GTATAGAGTCAGAAAGGTGGCTTCATTGAGACATGGAACCTTAACAAACAGCCATCCAGT 222
Qy 125 GGC CGCGGTGCGCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCCCTTCT 184
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Qy 185 ACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGAAAGGGGATATCTTTGGTGTGATAT 244
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Qy 305 AAAGACCACAGAGCGTCTCCAGGAGAAAGCCAAAGCCCAACAGCAACAGATAGTCACC 364
Db 375 -----CAACAAAAGGACAAAGCAGCAGCGCCCAAGACCGTACC 414
Qy 365 AGAAGGTGACCGCTTTTCGATGAGGGTGATCTCATTCAGTTCCACCGGTGTGTCTTCT 424
Db 415 AGAAGATCTATCATCTTCAGAGAGGGTGATTGATTCAGTGCCTCAACCGGTTTGCTACT 474
Qy 425 GGCTCTAACAGCAGCAGCAGTGTGTTGCTGCTTCTCTTACTGACACCAACAACA 484
Db 475 GGATGTACAAACAAATGAAGACACTCTCTGTTGTTGCTGCTTCTCTTATGACACCAACAGCT 534
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Db 535 TCCAGAACAGCTCGACAGATGCTTAGAGATTCTATCTTGTCTGGAAACCAAGACGACAG 594
Qy 545 AGTTCTTAAGGTACCAACCAAGAGCAGCAACAGCAGACGAAAGCTTACCATATAGCC 604
Db 595 AGTTCTTACAGTATCAGCCACAGACAGCAGCAAG----- 627
Qy 605 CATACAGCCCGCAAGTACGCTAGACAAAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
Db 628 -----GAGGTACTC 636
Qy 665 ACAGCGCAGAGAACCGCAGGAGCAAGAAAGAAAGAAAGGTGGAACATCTTCAGCG 724
Db 637 AAAGCCAGAAAGGAAAGCGTCACCAAGAGAGAAAGAAAGAGGAGCAGCATATTGAGTG 696
Qy 725 GCTTACGCGCGGAGTTCTTGAAACAAAGCTTCCAGTTTGACGACAGCAGATAGTGCAAA 784
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Qy 965 ATGGTATTGAAGAGACGATCTGCACCGCAAGTGTCTAAAAAGAACATTTGGTAGAAACAGAT 1024
Db 919 ATGGCATTGACGAGACCAATTTGCACATGAGACTTCCGCACACATTTGGCCAGACTTCAT 978
Qy 1025 CCCTGACATCTACAAACCCCTCAAGCTGAGTGTTCATCTCAAAACTGCGAACAGTCTCAACCTTC 1084
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Qy 1385 CCCTCATAGATAACCTCGCGGAGAGTGTTCGAAATTCATATGCGCTTCCAAAGGGAGC 1444
Db 1339 CATTTGTTGAACGATTTCGCGGAGAGTGTATTCAGCAAACTTTAACTTAAGGAGCGAGC 1398
Qy 1445 AGCAGAGGAGCTTAAGACAAACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGT 1504
Db 1399 AGCCAGGCGAGGTCAAGAACAAACCCCTTTCAGCTTTCCTGGTTCCACCTTAAGGAGTCTC 1458
Qy 1505 CTCGAGGGCTGTGGCTTA 1523
Db 1459 AGAGGAGAGTTGTGGCTTA 1477

RESULT 14
ID ADX13008
XX ADX13008 standard; cDNA; 1697 BP.
AC ADX13008;
XX
XX 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 7583.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactonnanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
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PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
XX Claim 1; SEQ ID NO 7583; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactonnanan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1697 BP; 505 A; 410 C; 397 G; 385 T; 0 U; 0 Other;
Query Match 34.0%; Score 517.4; DB 13; Length 1697;
Best Local Similarity 62.8%; Pred.No.1.8e-117;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;
Qy 5 AGCAACCGGAGGAGAACGGTGCAGTTCAGCGCTCAATGCGCAGACCTTGACAATC 64
Db 106 AGCAGCCACAGCAAAACGAGTGCAGATCCAAAGCTCAATGCCCTCAAAACCGATAACC 165
Qy 65 GCATTGAATCAGAGGCGGTTCATTGAGACTTTGGAACCCCAACCAACAGGAGTTGCAAT 124
Db 166 GTATAGAGTCAGAAAGGTGGCTTCATTGAGACATGGAACCCCTAACACAAGCCATTCCAGT 225
Qy 125 GCGCGGCGTCCCTCTCTCGTTCAGTCTCGCGCAACGCCCTTCGTAGGCCCTTCT 184
Db 226 GTGCGCGGTTCGCTCTCTCGTTCAGTCTCGCGCAACGCCCTTCGAGACCTTCT 285
Qy 185 ACTCAATCTCTCCAGGAGATCTTCATCCAGCAAGAAAGGGGATATCTTTGGTGTGATAT 244
Db 286 ACACCAACCTCTCCAGGAGATCTACATCCAAACAGTAGTGTATTTTGGCATGATAT 345
Qy 245 TCCCTGGTGTCTCTAGACACTATGAAGAGCGCTCACACACAAGTCTCGATCTCAGTCCC 304
Db 346 TCCCGGGTGTCTCTAGACACTTTGAAGAGCT----- 377
Qy 305 AAAGACCACCAAGAGCTCTCCAAAGGAGAGACCAAGCCCAACAGCAACGAGATGATCACC 364
Db 378 -----CAACAAAAGAGCAAAAGAGAGCGGCCCAAGACCGTCAAC 417
Qy 365 AGAAGGTGCACCGTTTTCGATGAGGGTGTATCTCATTCAGTTCCTCCACCGGTGTGTTCT 424
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Qy 425 GGCCTCTAGAACGACCAACGACACTGATGTGTTGTTGTTCTCTTACTGACCAACCAACA 484
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Db 478 GGATGTACAACATGAAGACATCTCTGTTGTTGCCGTTTCTCTTATTGACACCAACAGCT 537
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QY 545 AGTTCTTAGGTACAGCAACAAGACAGACAAAGACAGACGAAGACGCTTACCATATAGCC 604
Db 598 AGTTCTTAGGTACAGCAACAAGACAGACAAAGACAGCAAG- 630
QY 605 CATACAGCCGCAAGTCCAGCTAGACAAAGAGAGCGTGAAATTAGCCCTCGAGGACAGC 664
Db 631 -----GAGGTACTC 639
QY 665 ACAGCCGACAGAAACGAGCAGGACAGAAAGAAACGAAGGTGGAACATCTTCAGCG 724
Db 640 AAAGCAGAAAGGAAGCGTCAGCAAGAAAGAAACGAAGGAGGACGATATTGAGTG 699
QY 725 GCTTCAGCGCGAGTTCTCGAACCAAGCCTTCCAGGTTGACGACACAGATAGTCAAA 784
Db 700 GCTTCGCCCCGAATTCCTTGAACATGCGTTC---GTCGTGGACAGCGAGATAGTGAGAA 756
QY 785 ACCTAAGAGCGAGACGACGAGTGAAGAGAGGAGCCATTGTGACAGTCAAGGAGGCGC 844
Db 757 AGCTACAAGTGAGACGAAGAGAGAGAGAGAGGTTGCCATTGTGACAGTGAAGAGGTC 816
QY 845 TCAGAAATCTTGAGCCAGATAGAAAGAGAGAGCTGCCAGCAAGAGGAATACGATGAG 904
Db 817 TCAGCGTGATAGCCCAACCCAGGAGAGCAGCAACAAGAGCCGAGGAAGAGGAGAAGC 876
QY 905 ATCAATATGAATACGATAGAGAGATAGAGGCGTGGCAGGGAAGCAGAGGAGGGGA 964
Db 877 CAGATTGTGACGAGAAAGCAAAACAT-----TGCCAAAGCCAAAGCAGAA 921
QY 965 ATGGTATTGAAGACAGATCTGCACCGCAAGTGCTAAAGAAAGACATTTGGTAGAAACAGAT 1024
Db 922 ATGGCATTGACGAGACCAATTTGCACATGAGACTTCGCCACACATTTGCCAGACTTCAT 981
QY 1025 CCCTGACATCTACAAACCTTCAAGCTGGTTCACTCAAAAAGTCCAAAGATCTTCAACCTTC 1084
Db 982 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACCGCTACGAGCTCGACTTC 1041
QY 1085 TATATCTTAGTGGCTTGGACCTAGTGTGAATATGMAATCTTACAGGAATGCATTGT 1144
Db 1042 CAGCCCTCTGCTGGCTCAAACTCAGTGCCCAAGTTTGGATCACTCCGCAAGATGCTATGT 1101
QY 1145 TTGTCGCTCACTACAAACCAACGACACACAGCATCATATATCGATTGAGGGGACGGGCTC 1204
Db 1102 TCGTGCCACACTACACCTGAACGCAACAGCATATATATACGCAATTGMAATGGACGGCAT 1161
QY 1205 ACGTGAAGTCGTGGACAGCAACGCGCAACAGAGTGTACGAGGAGGCTTCAAGAGGGTC 1264
Db 1162 TGGTACAAGTGGTGAATTGCAATGGTGAGAGAGTGTGATGAGAGAGCTGCAAGAGGGAC 1221
QY 1265 ACGTGTCTGTGGGCCACAGAACTTCGCGCTGCTGGAAGTCCAGAGGAGCAACTTCG 1324
Db 1222 AGGTGTAAATGTGGCCACAAAACCTTTGCGGTGGCTGCAAGATCACAGAGCCACACTTCG 1281
QY 1325 AATACGTGGCATTCAGACAGACTCAAGGCGCCAGCATAGCAACCTCGCGGTGAAAACT 1384
Db 1282 AGTATGTTTCAATTCAGACCAATGATAGACCCCTCGATCGGCAACCTTGCAAGGTGCAAACT 1341
QY 1385 CCGTCATAGATAACCTGCGGAGAGAGGTGGTTCGAATTCATATGCGCTCCAAAGGAGC 1444
Db 1342 CATTTGTGAACGCAATTCGCGGAGAGAGTGATTCAGCAAACTTTTAAACCTTAAGGAGCGAC 1401
QY 1445 AGCAGGCGAGCTTAAGAACAAACCCCTTCAAGTTCTTCAAGTTCTTCAACCGCTCTCAGCAGT 1504
Db 1402 AGCCAGGCGAGGTCAGAGAACAAACCCCTTTCAGTTCTTGGTTCCACCTTAAGAGTCTC 1461
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Db 1462 AGAGGAGAGTGTGGCTTA 1480

RESULT 15
ADX13019
ID ADX13019 standard; cDNA; 1671 BP.

XX AC ADX13019;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 7594.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TAB/) TABASKA J E.
XX PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX Claim 1; SEQ ID NO 7594; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
XX invention.

XX SQ Sequence 1671 BP; 498 A; 404 C; 396 G; 373 T; 0 U; 0 Other;
Query Match 33.8%; Score 515.8; DB 13; Length 1671;
Best Local Similarity 62.7%; Pred. No. 5.2e-137;

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 09:32:31 ; Search time 7832.57 Seconds
(without alignments)
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Title: US-10-728-051-3

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*
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4: gb_est5:*
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6: gb_hsc:*
7: gb_est3:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_ges1:*
12: gb_ges2:*
13: gb_ges3:*
14: gb_ges4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	604.4	39.7	725	4	CD038327	CD038327 UTPPI008
3	562.2	36.9	676	4	CD038254	CD038254 UTPPI004
4	554.6	36.4	710	4	CD038107	CD038107 UTPPI002
5	548.6	36.0	718	4	CD038332	CD038332 UTPPI004
6	487	32.0	553	8	CO897496	CO897496 EST00001
7	436	28.6	602	4	CD038301	CD038301 UTPPI005
8	417.6	27.4	532	4	CD038222	CD038222 UTPPI004
9	386.2	25.3	720	4	CD038043	CD038043 UTPPI001
10	373.6	24.5	452	8	CO897497	CO897497 EST00002
11	372	24.4	679	4	CD038144	CD038144 UTPPI003
12	330.4	21.7	906	3	BQ123409	BQ123409 EST608985
13	321.6	21.1	974	3	BQ123283	BQ123283 EST608859
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15	314	20.6	861	4	CA858492	CA858492 EST635747
16	310.6	20.4	810	4	CA858379	CA858379 EST635634
17	310.4	20.4	862	4	CA858208	CA858208 EST635463
18	310.2	20.4	907	3	BQ123241	BQ123241 EST608817
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25	302.6	19.9	881	4	CA858490	CA858490 EST635745
26	298.4	19.6	790	4	CA858419	CA858419 EST635674
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37	288.6	18.9	746	2	B1311303	B1311303 EST531305
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45	285.2	18.7	796	4	CA857752	CA857752 EST635007

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION UTPPI007 B05 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI007_B05 5', mRNA sequence.
ACCESSION CD038329.1 GI:30420167
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Arachis hypogaea (peanut)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.
REFERENCE 1 (bases 1 to 770)
AUTHORS Luo M., Dang P., Guo B.Z., Holbrook C.C., Lee R.D., Bausher, M.G. and Lynch R.E.
TITLE Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL Unpublished (2003)
COMMENT Contact: Baozhu Guo
Molecular Genetics
USDA/ARS Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.

FEATURES

source
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Al3"
/db_xref="taxon:3818"
/clone="UTPP1007_B05"
/tissue_type="Immature pods"
/dev_stage="R6"
/lab_host="xL1-blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar Al3 (NCV11XAR4). Al3 has resistance to Aspergillus infection


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157 AATGCGCGCGCGCTCTCTCGCTTAGTCTCCGCCGCAACGCCCTTCGTAGGCGTT 216
182 TCTACTCCAATGCTCCCGCAGGAGATCTTCATCGACGAAGGAAGGAGATCTTTGGGTTGA 241
217 TCTACTCCAATGCTCCCGCAGGAGATCTTCATCCAGCAAGGAAGGAGATCTTTGGTTTGA 276
242 TATTTCCTCGTGTCTCTAGACACTATGAAGAGCTCACACACAAAGTCTCGATCTCAGT 301
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337 CCCAAGAGACCACCAAGAGCTTTTCAAGGACAAGACCAAAAGCCCAACAGCAAGATAGTC 396
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517 ACAACGACAAACAGCTTTGATCAGTTCGCCAGGAGATTCAATTTGGCTGGGAACACGAGC 576
542 AAGAGTTCTTAAGGTACCAACCAAGACAGCAAAAGCAGACAGAAAGAGCTTACCATATA 601
577 AAGAGTTCTTAAGATACCAGCA-----ACAAAGCAGACAGAAAGAGCTTACCATATA 627
602 GCCCATACAGCCCGCAAGTTCAGCTAGACAAAGAGAGCTGTAATTTAGCCCTCGAGGAC 661
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662 AGCACAGCCGACAGAAACGACGAGGACCAAGAAAGAA 699
688 AGCAGCGCGCAGACAGACGAGGACAGCAAGAAACAGAA 725

RESULT 3
CD038254
LOCUS
DEFINITION
UTPPI004_F06 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
Arachis hypogaea cDNA clone UTPPI004_F06 5', mRNA sequence.
ACCESSION
CD038254
VERSION
CD038254.1 GI:30420092
SOURCE
Arachis hypogaea (peanut)
ORGANISM
Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
REFERENCE
1 (bases 1 to 676)
Luo M., Dang P., Guo B.Z., Holbrook, C.C., Lee, R.D., Bausher, M.G.
and Lynch, R.E.
Generation and Analyses of ESTs for Arachis hypogaea
Unpublished (2003)
COMMENT
Contact: Baozhu Guo
USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.
FEATURES
source
location/Qualifiers
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/dev_stage="R6"
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/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
(UTPP)"
/notes="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NCv11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure(GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
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ORIGIN

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Query Match      36.9%; Score 562.2; DB 4; Length 676;
Best Local Similarity 92.2%; Pred. No. 1.2e-143;
Matches 630; Conservative 0; Mismatches 38; Indels 15; Gaps 3;

QY 538 GAGCAGAGGTTCTTAGGTACCAGCAACAAAGCAGACAGAAAGCAGACGAGCAAGAGCTTACCA 597
Db 3 GAGCAAGAGTTCTTAAGATACCAGCAACAAAGCAGACAGAAAGCAGACGAGCAAGAGCTTACCA 62
QY 598 TATAGCCCATACAGCCCGCAAGTTCAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGA 657
Db 63 TTAAGCCCATACAGCCC-----TCAGCCTGGACAAAGAGACCGTGAATTTAGCCCTCAA 116
QY 658 GGACAGCAGCGCCGACAGAGAAAGCAGACAGAAAGAGAAAGAAAGAGAGTGAAGCAATC 717
Db 117 GGACAGCAGCGCGCAGAGAGAAAGCAGACAGAAAGAGAAAGAAAGAGAGTGAAGCAATC 176
QY 718 TTCAGCGGCTTCACGCCGAGGTTCTTGGAAACAGCCTTCAGGTTTCACGACACAGAGATA 777
Db 177 TTCAGCGGCTTCACGTCGGAGTCTCTGGCACAAGCCCTTCAGGTTTCACGACACAGAGATA 236
QY 778 GTGCAAAACCTTAAGAGCGCAGACCGAGAGTGAAGAAAGAGGAGGCCATTTGTACAGTGAGG 837
Db 237 GTGCAAAATCTAAGAGCGCAGAAACAGAGAGTGAAGAAACAGGAGGCCATTTGTACAGTGAAG 296
QY 838 GGAGGCTCAGAAATCTTGAGCCAGATGAAGAGAGAGCTGCCGACCAAGAGAGGAATAC 897
Db 297 GGAGGCTTCAGAAATCTTGAGCCAGATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGATAC 353
QY 898 GATGAAGATGAATATGAATACGATG-----AAGAGGATAGAGGCGTTCGACGGGAAGC 951
Db 354 GATGAAGACGAATATGCTGAAGAGGAGAGGCAACAAAGATAGAAAGGCGTTCGACGGGAAGC 413
QY 952 AGAGGCGAGGGGAATGGTATTGAAGAGAGAGATCTGCACCAGCAAGTGTCTAAAAAGAACATT 1011
Db 414 AGAGGCGAGCGCAATGGCATTGAGGAGACCATCTGCACCAGCAATCTTAAAAAGAACATT 473
QY 1012 GGTAGAAACAGATCCCTCAGATCTTACACCCCTCAAGCTGGTGTCTCACTCAAAACTGCAAC 1071
Db 474 GGTAGAAACAGATCCCTCAGATCTTACACCCCTCAAGCTGGTGTCTCACTCAAAACTGCAAC 533
QY 1072 GATCTCAACCTTCTAATACCTTAGGTGGCTTGGACCTAGTGAATATGGAATCTCTAC 1131
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QY 1132 AGGAATGCATTGTTTCTCCTCACTACAAACCGCACAGCATATATATCGATTG 1191
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Db 594 AGGAATGCATTGTTTCTCCTCACTACAAACCGCACAGCATATATATCGATTG 653
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QY 1192 AGGGACGGGCTCACGTGCAAGT 1214
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Db 654 AGGGACGGGCTCATGTGCNAGT 676
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RESULT 4
CD038107 710 bp mRNA linear EST 07-MAY-2003
LOCUS UTPPI002_E08 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
DEFINITION Arachis hypogaea cDNA clone UTPPI002_E08 5', mRNA sequence.
CD038107
ACCESSION CD038107.1 GI:30419945
VERSION EST.
KEYWORDS Arachis hypogaea (peanut)
SOURCE Arachis hypogaea

ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 710)

REFERENCE 1
AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
TITLE Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL Unpublished (2003)
COMMENT Contact: Baozhu Guo
Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3

FEATURES
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1..710
/organism="Arachis hypogaea"
/mol_type="mRNA"
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/lab_host="XLI-Blue"
/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
/note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13;
(NCVLIx4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lambda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN
Query Match 36.4%; Score 554.6; DB 4; Length 710;
Best Local Similarity 98.3%; Pred. No. 1.6e-141;
Matches 571; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 945 GGGACGAGCAGCGGGGAATGGTATTGAAGAGAGATCTGCACCGCAAGTGCTAAAAA 1004
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Db 1 GGGACGAGCAGCGGGGAATGGTATTGAAGAGAGATCTGCACCGCAAGTGCTAAAAA 60
|||||
QY 1005 GAACATTGTTAGAAAACAGATCCCTTGACATCTACAAACCTCAAGCTGGTTCACTCAAAAC 1064
|||||
Db 61 GAACATTGTTAGAAAACAGATCCCTTGACATCTACAAACCTCAAGCTGGTTCACTCAAAAC 120
|||||
QY 1065 TGCCAACGATCTCAACCTTCTAATATTAGGTGGCTTGGACCTAGTGTGTAATATGAAA 1124
|||||
Db 121 TGCCAACGATCTCAACCTTCTAATATTAGGTGGCTTGGACCTAGTGTGTAATATGAAA 180
|||||
QY 1125 TCTCTACGGAATGCATTGTTGTGCTCACTACAAACCAACGACACAGCATATATA 1184
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Db 181 TCTCTACGGAATGCATTGTTGTCTCTACTACAAACCAACGACACAGCATATATA 240
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Db 241 TCGATTGAGGGACCGGGCTCACGTGCAAGTCGTGGACAGCAACGGCCACAGAGTGACGA 300
|||||
QY 1245 CGAGGAGCTTCAAGAGGGTCAGTGTGTTGGTCCACAG-ACTTCGGCGTGGCTGGAA 1303
|||||
Db 301 CGAGGAGCTTCAAGAGGGTCAGTGTGTTGGTCCACAGNAACCTTCGCCGTGGCTGGAA 360
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QY 1304 AGTCCGAGAGCAGAACTTTCGAATACGTGGCATTTCAAGACAGACTCAAGGCCACGATAG 1363
|||||
Db 361 AGTCCGAGAGCAGAACTTTCGAATACGTGGCATTTCAAGACAGACTCAAGGCCACGATAG 420
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QY 1364 CCAACCTCGCCGGTGAAAACTCCGTCATAGATAAACCCTCGGAGGAGGTGGTTGCAAAAT 1423
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Db 421 CCAACCTCGCCGGTGAAAACTCCGTCATAGATAAACCCTCGGAGGAGGTGGTTGCAAAAT 480
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QY 1424 CATATGGCTTCCMAAGGAGAGCGGCAAGCAGCTTAAAGAACAAACCCCTTCAAGTTCT 1483
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Db 481 CATATGGCTTCCMAAGGAGAGCGGCAAGCAGCTTAAAGAACAAACCCCTTCAAGTTCT 540
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QY 1484 TCGTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 1524
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Db 541 TCGTTCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 581
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RESULT 5
CD038332 718 bp mRNA linear EST 07-MAY-2003
LOCUS UTPPI004_B04 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
DEFINITION Arachis hypogaea cDNA clone UTPPI004_B04 5', mRNA sequence.
CD038332
ACCESSION CD038332.1 GI:30420170
VERSION EST.
KEYWORDS Arachis hypogaea (peanut)

SOURCE Arachis hypogaea
ORGANISM Arachis hypogaea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 718)

REFERENCE 1
AUTHORS Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
and Lynch,R.E.
TITLE Generation and Analyses of ESTs for Arachis hypogaea
JOURNAL Unpublished (2003)
COMMENT Contact: Baozhu Guo
Molecular Genetics

USDA/ARS, Crop Protection and Management Research Unit
2747 Davis Rd., Tifton, GA 31794, USA
Tel: 229-387-2334
Fax: 229-387-2321
Email: bguo@tifton.usda.gov
Seq primer: T3.

FEATURES
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/organism="Arachis hypogaea"
/mol_type="mRNA"
/cultivar="A13"

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/db_xref="taxon:3818"
/clone="UTPP1004_B04"
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/dev stage="R6"
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/clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
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/notes="vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI;
cDNA library was constructed from peanut cultivar A13
(NC11XAR4). A13 has resistance to Aspergillus infection
and drought tolerance. The immature pods that developed to
R6 stage were collected from different plants, and placed
into liquid N2 immediately and stored in -80oC freezer.
Total RNA was isolated with TRIzol-Reagent
ultrapure (GIBCOBRL). mRNA was extracted and purified from
total RNA (Promega). cDNA synthesis and library
construction followed the protocol of by ZAP-cDNA Gigapack
III Gold cloning kit (Stratagene). The cDNA above 500bp
were collected after size-fraction. The inserts were
directionally cloned into Uni-ZAP XR vector using XhoI
EcoRI sites adapters. The lamda library was packed into
phages using Gigapack III Gold (Stratagene). The
un-amplified library was used to excise pBluescript
phagemids from the Uni-ZAP XR vector, and the phagemids
was used to transform the host bacteria SOLR. The library
was constructed by Dr. Meng Luo and Dr. Phat Dang."
```

ORIGIN

Query Match 36.0%; Score 548.6; DB 4; Length 718;
Best Local Similarity 93.4%; Pred. No. 7.3e-140;
Matches 621; Conservative 0; Mismatches 29; Indels 15; Gaps 4;

QY 875 GTGCCACGAAGAGGAAATACGATGAAGATGAATATGAATACGATGAAGAG----- 927
DB 1 GTCCCGACGAAGAGGATACGATGAAGATGAATATGAATATGAATGAGAGGAGGC 60

QY 928 -----GATGAAGCGTGGCAGGGGAAGCAGAGCGAGGGGAATGGTATTGAAGAGACGA 982
DB 61 AACAAATAGAAAGCGTGGCAGGGGAAGCAGAGCGAGCGCAATGGCATTTGAGGAGACCA 120

QY 983 TCTGCAACCGAAGTCTTAAAGAAACATTTGGTGAAGACAGATCCCTGACATCTACAACC 1042
DB 121 TCTGCAACCGAAGTCTTAAAGAAACATTTGGTGAAGACAGATCCCTGACATCTACAACC 180

QY 1043 CTCAGCTGGTTCACTCAAAATGCCAACCGATCTCAACCTTCTAATACTTAGTGGCTTG 1102
DB 181 CTCAGCTGGTTCACTCAAAATGCCAACCGAGTCAACCTTCTAATCTTAGTGGCTTG 240

QY 1103 GACCTAGTGTGAATATGGAAATCTCTACAGGAATGCATTTGTTGGCTCACTACAACA 1162
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QY 1163 CCACCGCACACGATCATATATCGATTGAGGGAGGGGCTCAGTGCAGTCTGTCGACCA 1222
DB 301 CGAACCGCACACGATCATATATCGATTGAGGGAGGGGCTCAGTGCAGTCTGTCGACCA 360

QY 1223 GCAACGGCAACACAGTGTACGACGAGGAGTTCACAGAGGGTCACTGCTTGTGGTGGCAC 1282
DB 361 GCACCGGCACACAGTGTTCGACGAGGAGTTCACAGAGGTCACTGCTTGTGGTGGCAC 420

QY 1283 AG-AACTTCGCGTGGTGAAGAGTCCAGAGCGAGAACTTCGAATACGTTGGCATTCAG 1341
DB 421 AGAAACTTCGCGTGGTGAAGAGTCCAGAGCGAGAACTTCGAATACGTTGGCATTCAG 480

QY 1342 ACAGACTCAAGGCCACGATAGCAACCTCGCGGTGAAACCTCCCTCATAGATACCTTG 1401
DB 481 ACAGACTCAAGGCCACGATAGCAACCTCGCGGTGAAACCTCCCTCATAGATACCTTG 540

QY 1402 CC--GGAGGAGGTGGTGCATAATTCATATGGCCCTCCAAAGGGAGCAGGAGGCGCTTAA 1460
DB 541 CCGGGAGGAGGTGGTGCATAATTCATATGGCCCTCCCAAGGGAGCAGGAGGCGCTTAA 600

QY 1461 GAACAAACA--CCCTTTCAAGTCTTCTGTTCCACCGTCTCAGCAGTCTCCGAGGGCTGTG 1519

Db 601 GAACAACAACCCCTTCAAGTCTTCTGTTCCACCGTCTCAGCAGTCTCTGAGGCTGTGG 660

QY 1520 CTTAA 1524

Db 661 CTTAA 665

RESULT 6
CO897496

LOCUS CO897496

DEFINITION Peanut Lambda Express library Arachis hypogaea cDNA 5', mRNA sequence.

ACCESSION CO897496

VERSION CO897496.1 GI:51237286

KEYWORDS EST.

SOURCE Arachis hypogaea (peanut)

ORGANISM Arachis hypogaea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae; Arachis.

REFERENCE 1 (bases 1 to 553)
Yan, Y.S.; Wang, L.; Zhong, Y.J. and Huang, S.Z.
Expressed sequence tags of mid-matured cotyledons of peanut
Unpublished (2004)
Contact: Shangzhi Huang
Plant Development and Molecular Biology
Sun Yat-sen University, Department of Biology and Biotechnology
Guangzhou, 510275, China
Tel: (860) 02084036592
Email: yys9803@yahoo.com.cn
Seq primer: pTriplEx2 Forward.
Location/Qualifiers
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/organism="Arachis hypogaea"
/mol_type="mRNA"
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/db_xref="taxon:3818"
/tissue type="Cotyledons"
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/clone_lib="Peanut Lambda Express library"
/notes="Organ: Seed; Vector: lambdaTriplEx2"

ORIGIN

Query Match 32.0%; Score 487; DB 8; Length 553;
Best Local Similarity 93.8%; Pred. No. 7.1e-123;
Matches 508; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 39 CCTCAATGCGCAGAGACCTGACAAATCGCATTTGAATCAGAGGGCGGTTACATTGAGACTTG 98
DB 1 CCTCAATGCGCAAGCGCTTGACAAACCGCATTTGAATCGAGGGCGGTTACATTGAGACTTG 60

QY 99 GAACCCCAACAACAGAGAGTTGAAATGCGCGCGCTGCGCCCTCTCTCGTTAGTCTCCG 158
DB 61 GAACCCCAACAACAGAGAGTTGAAATGCGCGCGCTGCGCCCTCTCTCGCTTAGTCTCCG 120

QY 159 CGCAGACGCCCTTCGTAGGCGCTTCTACTCCAAATGCTCCCGAGAGATCTTCATCCAGCA 218
DB 121 CGCAGACGCCCTTCGTAGGCGCTTCTACTCCAAATGCTCCCGAGAGATCTTCATCCAGCA 180

QY 219 AGAAGGGGATCTCTTTGGGTGTGATATTCCTCGTGTCTCTAGACACTATGAAGAGCTCA 278
DB 181 AGAAGGGGATCTCTTTGGGTGTGATATTCCTCGTGTCTCTAGACACTATGAAGAGCTCG 240

QY 279 CACACAAGGTGCTCGATCTCTAGTCCCAAGAGACCAACCAAGAGCTCTCAAGGAGAGACCA 338
DB 241 ACAACAAGGACGCCGACATCAGTCCCAAGAGACCAACCAAGAGCTCTTCAGAGGACCA 300

QY 339 AAGCCCAACGACGAGATAGTACCAGAGGTGCAACCGTTTCGATGAGGGTGTATCTCAT 398
DB 301 AAGCCCAACGACGAGATAGTACCAGAGGTGCAACCGTTTCGATGAGGGTGTATCTCAT 360

399 TGAGTCCACCGGTGTTGCTTTCTGGCTCTACAAAGCAGCAGCACTGATGTTGTC 458
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 361 TGCAGTCCACCGGTGTTGCTTTCTGGATGTACAAAGCAGCAGCACTGATGTTGTC 420
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 459 TGTTCCTCTACTGACACCAACACACGACACAGCAGCTTGATCAGTTCCTCCAGGAGATT 518
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 421 TGTTCCTCTACTGACACCAACACACGACACCAACAGCTTGATCAGTTCCTCCAGGAGATT 480
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 519 CAATTGGCTGGGAACACGAGCAAGAGTTCCTTAAGGTACCAAGCAAAAGACAGACAAAG 578
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 481 CAATTGGCTGGGAACACGAGCAAGAGTTCCTTAAGATACCAACACAAAGACAGACGAG 540
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 579 CAG 581
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 541 AAG 543

RESULT 7
 CD038301
 LOCUS
 DEFINITION
 Arachis hypogaea cDNA clone UTPI005_C08 5', mRNA sequence. EST 07-MAY-2003
 Arachis hypogaea (peanut)
 Arachis hypogaea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
 Aeschynomeneae; Arachis.
 1 (bases 1 to 602)
 Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
 and Lynch,R.E.
 Generation and Analyses of ESTs for Arachis hypogaea
 Unpublished (2003)
 Contact: Baozhu Guo
 Molecular Genetics
 USDA/ARS, Crop Protection and Management Research Unit
 2747 Davis Rd., Tifton, GA 31794, USA
 Tel: 229-387-2334
 Fax: 229-387-2321
 Email: bguo@tifton.usda.gov
 Seq primer: T3.
 Location/Qualifiers
 1. .602
 /organism="Arachis hypogaea"
 /mol_type="mRNA"
 /cultivar="A13"
 /db_xref="taxon:3818"
 /clone="UTPI005_C08"
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 /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library
 (UTPP)"
 /notes="Vector: Uni-ZAP XR; Site1: EcoRI; Site 2: XhoI;
 cDNA library was constructed from peanut cultivar A13
 (NCV11XAR4). A13 has resistance to Aspergillus infection
 and drought tolerance. The immature pods that developed to
 R6 stage were collected from different plants, and placed
 into liquid N2 immediately and stored in -80°C freezer.
 Total RNA was isolated with TRIzol-Reagent
 ultrapur (GIBCOBRL). mRNA synthesis and library
 total RNA (Promega). cDNA synthesis and library
 construction followed the protocol of by ZAP-cDNA Gigapack
 III Gold cloning kit (Stratagene). The cDNA above 500bp
 were collected after size-fraction. The inserts were
 directionally cloned into Uni-ZAP XR vector using XhoI
 EcoRI sites adaptors. The lambda library was packed into
 phages using Gigapack III Gold (Stratagene). The
 un-amplified library was used to excise pBluescript

FEATURES
 source

ORIGIN

Query Match 28.6%; Score 436; DB 4; Length 602;
 Best Local Similarity 95.7%; Pred. No. 9.1e-109; Indels 0; Gaps 0;
 Matches 448; Conservative 0; Mismatches 20;
 QY 1057 CTCAAATCGCCAAACGATCTCAACCTTCTTAATCTTAGTGGCTTGGACCTAGTGTGAA 1116
 DB 1 CTCAAATCGCCAAACGAGCTCAACCTTCTTAATCTTAGTGGCTTGGACCTAGTGTGAA 60
 QY 1117 TATGGAATCTCTACAGGAATGATTTGTCGCTACTACACACCAACGACACAGC 1176
 DB 61 TATGGAATCTCTACAGGAATGATTTGTCGCTACTACACACGACACAGC 120
 QY 1177 ATCATATATCGATTGAGGGACGGCTCACGTGCAAGTCGTGCACAGCAACGCAACAGA 1236
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 QY 1237 GTGTACGACGAGAGCTTCAAGAGGTCACGTGCTTGTGTCGCCACAGAACTTCGCCGTC 1296
 DB 181 GTGTCGACGAGAGCTTCAAGAAGTCACGTGCTTGTGTCGCCACAGAACTTCGCCGTC 240
 QY 1297 GCTGGAAGTCCAGAGCGAGAACTTCGAATACGTGGCACTCAAGACAGACTCAAGSCCC 1356
 DB 241 GCTGGAAGTCCAGAGCGAGAACTTGAATACGTGGCACTCAAGACAGACTCAAGSCCC 300
 QY 1357 AGCATAGCCAACTCCGCCGTGAAAACCTCCGTCATAGATAAAGCTCCGCGAGAGGTGGTT 1416
 DB 301 AGCATAGCCAACTAGCCGGTGAAAACCTCTTCATAGATAAAGCTCCGCGAGAGGTGGTT 360
 QY 1417 GCAATATCATATGGCTTCCAAAGGAGCAGGCAAGCAGCTTAAGAAACAAACACCCCTTC 1476
 DB 361 GCAATATCATATGGCTTCCAAAGGAGCAGGCAAGCAGCTTAAGAAACAAACACCCCTTC 420
 QY 1477 AGTTCCTTCGTTCCACCGTCTCAGCAGTCTCCGAGGGCTGTGGCTTAA 1524
 DB 421 AAGTTCCTTCGTTCCACCGTCTCAGCAGTCTCTGAGGGCTGTGGCTTAA 468

RESULT 8
 CD038222

LOCUS
 DEFINITION
 Arachis hypogaea cDNA clone UTPI004_B11 5', mRNA sequence.
 CD038222
 CD038222.1 GI:30420060
 EST
 Arachis hypogaea (peanut)
 Arachis hypogaea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
 Aeschynomeneae; Arachis.
 1 (bases 1 to 532)
 Luo,M., Dang,P., Guo,B.Z., Holbrook,C.C., Lee,R.D., Bausher,M.G.
 and Lynch,R.E.
 Generation and Analyses of ESTs for Arachis hypogaea
 Unpublished (2003)
 Contact: Baozhu Guo
 Molecular Genetics
 USDA/ARS, Crop Protection and Management Research Unit
 2747 Davis Rd., Tifton, GA 31794, USA
 Tel: 229-387-2334
 Fax: 229-387-2321
 Email: bguo@tifton.usda.gov
 Seq primer: T3
 Location/Qualifiers
 1. .532
 /organism="Arachis hypogaea"
 /mol_type="mRNA"

FEATURES
 source

phagemids from the Uni-ZAP XR vector, and the phagemids
 was used to transform the host bacteria SOLR. The library
 was constructed by Dr. Meng Luo and Dr. Phat Dang."

/cultivar="A13"
 /db_xref="taxon:3818"
 /clone="UTPPI004_B11"
 /tissue_type="Immature pods"
 /dev_stage="R6"
 /lab_host="Xli-blue"
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 /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 27.4%; Score 417.6; DB 4; Length 532;
 Best Local Similarity 96.8%; Pred. No. 1.1e-103;
 Matches 426; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1085 TAATACTTAGTGGCTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCATTGT 1144
 DB 1 TAATCTTGTAGTGGCTTGGACTTAGTCTGAATATGGAATCTCTACAGGAATGCATTGT 60

QY 1145 TTGTCTGCTACTCAACACCAACGACACACAGCATCATATATGATTGAGGGGACGGGCTC 1204
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QY 1205 ACGTGCAGTCTGTGGACAGCAACGCGACAGAGTGTACGACGAGGAGCTTCAAGAGGTC 1264
 DB 121 ACGTGCAAGTCTGTGGACAGCAACGCGACAGAGTGTACGACGAGGAGCTTCAAGAGGTC 180

QY 1265 ACGTGCTTGTGGTCCACAGCACTTCGCGCTGCTGGAAGTCCACAGAGGAGCACTTCG 1324
 DB 181 ACGTGCTTGTGGTCCACAGCACTTCGCGCTGCTGGAAGTCCACAGAGGAGCACTTCG 240

QY 1325 AATACGTGGCATTCAGACAGACTCAAGGCCCGACATAGCCAACTCGCGGTGAAACT 1384
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QY 1445 AGCAAGGAGCTTAAAGCAACACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGT 1504
 DB 361 AGCAAGGAGCTTAAAGCAACACCCCTTCAAGTCTTCGTTCCACCGTCTCAGCAGT 420

QY 1505 CTCGAGGGGCTGTGGCTTAA 1524
 DB 421 CTCGAGGGGCTGTGGCTTGA 440

RESULT 9

CD038043
 LOCUS 720 bp mRNA linear EST 07-MAY-2003
 DEFINITION UTPPI001_F09 USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)
 Arachis hypogaea cDNA clone UTPPI001_F09 5', mRNA sequence.
 ACCESSION CD038043
 VERSION CD038043.1 GI:30419881

KEYWORDS

SOURCE EST.

ORGANISM

Arachis hypogaea (peanut)
 Arachis hypogaea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae;
 Aeschynomeneae; Arachis.

REFERENCE

1 (bases 1 to 720)

AUTHORS

Luo, M., Dang, P., Guo, B. Z., Holbrook, C. C., Lee, R. D., Bausher, M. G.

TITLE

Generation and Analyses of ESTs for Arachis hypogaea

JOURNAL

Unpublished (2003)

COMMENT

Contact: Baozhu Guo
 Molecular Genetics
 USDA/ARS, Crop Protection and Management Research Unit
 2747 Davis Rd., Tifton, GA 31794, USA
 Tel: 229-387-2334
 Fax: 229-387-2321
 Email: bguo@tifton.usda.gov
 Seq primer: T3.

FEATURES

1..720
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 /organism="Arachis hypogaea"
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 /cultivar="A13"
 /db_xref="taxon:3818"
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 /tissue_type="Immature pods"
 /dev_stage="R6"
 /lab_host="Xli-blue"
 /clone_lib="USDA-Tifton Peanut Immature Pod cDNA Library (UTPP)"
 /note="Vector: Uni-ZAP XR; Site 1: EcoRI; Site 2: XhoI; cDNA library was constructed from peanut cultivar A13 (NCV11XAR4). A13 has resistance to Aspergillus infection and drought tolerance. The immature pods that developed to R6 stage were collected from different plants, and placed into liquid N2 immediately and stored in -80oC freezer. Total RNA was isolated with TRIZOL-Reagent ultrapure(GIBCOBRL). mRNA was extracted and purified from total RNA (Promega). cDNA synthesis and library construction followed the protocol of by ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The cDNA above 500bp were collected after size-fraction. The inserts were directionally cloned into Uni-ZAP XR vector using XhoI EcoRI sites adapters. The lambda library was packed into phages using Gigapack III Gold (Stratagene). The un-amplified library was used to excise pBluescript phagemids from the Uni-ZAP XR vector, and the phagemids was used to transform the host bacteria SOLR. The library was constructed by Dr. Meng Luo and Dr. Phat Dang."

ORIGIN

Query Match 25.3%; Score 386.2; DB 4; Length 720;
 Best Local Similarity 96.8%; Pred. No. 5.6e-95;
 Matches 394; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1118 ATGGAATCTCTACAGGAATGCATTGTTGCTCCTCACTACAACACCAACGACACAGCA 1177
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QY 1298 CTGGAAGTCCACAGACGAGAACTTCGAATACGTGTCATTCAAGACAGACTCAAGGCCCA 1357
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ORIGIN

/notes"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 25 to 35 days after pollination, were harvested from greenhouse-grown plants. Seed were removed and separated from pod walls and immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL10R cells."

OV 1225 AACGGCAACAGAGTGTACGACGAGGAGC^{TT}CAAGAGGGTCACGTGTCTGTGGTGCCACAG 1284

	Query Match	21.7%	Score 330.4	DB 3	Length 906
	Best Local Similarity	63.5%	Pred. No. 1.6e-79		
	Matches 540	Conservative 0	Mismatches 301	Indels 9	Gaps 2
Qy	680	GAGCAGACAAAGAAGAAACCAAGAGTGGAAACATCTTTCAGCGGCTTTCACGCCGGAGT	739		
Db	47	GAGAGAGGAAACAAACAGAAATATGAGGAGGCAACATTTTCAGTGGCTTTCAGAGGGATT	106		
Qy	740	TCCTGGAAACAAGCCTTTCAGGTTTCACACACAGACATAGTCGAAAACCTTAAGAGGCGAGA	799		
Db	107	TCTTGGAAGATGCATTGAACGTGA--ACAGGCATATAGTTGAAACACTTCAAGGCGAGGA	163		
Qy	800	CCGAGAGTGAAGAGAGGGAGCCATTGTGACGTAGGGGAGGCGCTCAGAACTCTTTGAGCC	859		
Db	164	ATGAAGACCAGGAGAGAGGGAGCCATTGTCAAAGTGGAAAGGAGACTCAGCATCTATGAGCC	223		
Qy	860	C-----AGATGAAAGAGACGTGCCACGAAAGAGAGGAATACGATGAAGATGAATATG	913		

RESULT 12

Dy
914 AAATCAGTGAAGGAGTAGAACCGCTGCACGGGGGAAACAGAGAGCAATGGATTG 375

Dz
284 ATGAGTGAGGCCACATCATCAGAAAAGCAGAAGAGAAAGAGAAAGGCACAACGGTCCTG 343

SEQUENCE: B0123409
ACCESSION

Db	CGAACAATTTGCATCGCAGGTTCCACAGAACATGGTCTCATCTTCATCACTGAC	403
Qy	TCTACAACCTCAAGCTGGTTCACTCAAACTGCCAACGATCTCAACCTTCTAATACTTA	1034
Db	TCTACAACCTCAAGCTGGTAGAATCAAAACTATACACAGCTTCGACCTCCAGCTCTCA	463
Qy	GGTGGCTTGACCTAGTGTGGAATATGGAATCTCTACAGGAATGCATGTGTTGTGCCTC	1153

REFERENCE 1 (pages 1 to 906)

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Qy	1214	TCGTGACAGCAACGGCCACACAGAGTGTACGACGAGGAGCTTCAAGAGGGTCACTGCTTG	1273
DB	584	TACTGAACTGCAATGGCAACACTGTGTTTCGATGAGGAACTAGAAGCTGGCCGTCATTGA	643

Email: ingrask@bell.liuc.edu
 MyCN community name: mycn.liuc.edu

644	DB	TCGTGCCACAAAACCTTTGCTGTTCGACGACAAAATCAGTGAGCGACAGGTTCACCTTATATGTTT	703
1334	QY	CATTCAAGGACAGACTCAAGGCCCGCAGATAGCCAACTTCGCGGTGAAAACTCCGTCATAG	1393
704	DB	CATTCAAGACCAATGATATATGCCGCAATTGCGAGGCTTGCGAGGACACAATCACCCTCAA	763
1394	QY	ATAACCTCGCGGAGGAGTGTTGCAATTCATATGGCCCTCCAAAGGACGAGCAGCAGGC	1453
764	DB	GTGGTATTCGCGATGTCGTTTGCAGCTACATTTCAACATGGACAGAAATGGAGCAGGC	823
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||| 1514 CTGTGGCTTA 1523
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RESULT 13
BQ123283
LOCUS
DEFINITION
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 974)
Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F. and Fraser, C.M.
ESTs from late stage developing seeds of Medicago truncatula
Unpublished (2002)
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713 798 7044
Fax: 713 798 7078
Email: mgrusak@bcm.tmc.edu
TIGR sequence name: MTRAO73TK More information is available at:
www.medicago.org
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/clone_lib="GLSP"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 25 to 35 days after pollination, were harvested from
greenhouse-grown plants. Seed were removed and separated
from pod walls and immediately frozen in liquid nitrogen.
Seeds throughout the age range were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in XL0LR cells."

ORIGIN
Query Match 21.1%; Score 321.6; DB 3; Length 974;
Best Local Similarity 63.7%; Pred. No. 4.4e-77;
Matches 524; Conservative 0; Mismatches 289; Indels 9; Gaps 2;

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QY 740 TCCTGGAAACAGGCTTCCAGGTTGACGACAGACAGATAGTGCAAAACCTTAAGAGCGGAGA 799
DB 162 TCTTGAAGATGCATTGAACGT--GAACGGCATATAGTTGAAAAACCTTCAAGGCAGGA 218
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DB 219 ATCAAGACCAGGAGAGGAGCCATTGTCAAAGTGGAAAGGAGACTCAGCATCATGAGCC 278
QY 860 C-----AGATAGAAAGAGACGCTGCCGACGAAGAGAGGAAATACGATGAAGATGAATATG 913
DB 279 CTCGAGAGAGACAAACACGCCACCCAGCAGACAGATGAAGAGATGAAGATGAAGAGG 338
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QY 974 AAGAGACGATCTGCACCGCAAGTGTAAAAAGAACATTTGGTAGAAACAGATCCCTTGACA 1033
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QY 1034 TCTACAAACCTCAAGCTGGTTCACTCAAAACCTGCCAACGATCTCAACCTTCTAATACTTA 1093
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QY 1094 GTGGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGGAATCATTTGTTTGTGCTC 1153
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QY 1454 AGCTTAAGAACAAACCCCTTCAAGTTCTTCTGTTCCACCGT 1495
DB 879 AGCTCAAAAACAACTCTCTTTAATTTCTAGTTTCAACCCCGT 920

RESULT 14
BQ123283
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Medicago truncatula (barrel medic)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 886)
Grusak, M.A., Samac, D., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F. and Fraser, C.M.
ESTs from late stage developing seeds of Medicago truncatula
Unpublished (2002)
Contact: Grusak, M.A.
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
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GenCore version 5.1.9
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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	517.4	34.0	1446	3	US-09-108-010B-13
3	517.4	34.0	1446	3	US-09-758-652-13
4	517.4	34.0	1446	3	US-10-684-651-13
5	513	33.7	1488	3	US-09-108-010B-11
6	513	33.7	1488	3	US-09-758-652-11
7	513	33.7	1488	3	US-10-684-651-11
8	513	33.7	1743	3	US-09-762-381-1
9	505	33.1	1746	3	US-09-805-694B-15
10	504	33.1	1458	3	US-09-108-010B-12
11	504	33.1	1458	3	US-09-758-652-12
12	504	33.1	1458	3	US-10-684-651-12
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14	198	13.0	1551	3	US-09-758-652-15
15	198	13.0	1551	3	US-10-684-651-15
16	153.2	10.1	1689	3	US-09-108-010B-14
17	153.2	10.1	1689	3	US-09-758-652-14
18	153.2	10.1	1689	3	US-10-684-651-14
19	142	9.3	1706	3	US-09-462-720-1
20	136.6	9.0	1685	2	US-08-486-721A-1
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22	132.2	8.7	1556	2	US-08-486-721A-2
23	114.6	7.5	3113	2	US-08-146-422-20

ALIGNMENTS

RESULT 1

US-09-715-036-4
; Sequence 4, Application US/09715036
; Patent No. 6943010
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/09/715, 036
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-09-715-036-4
Query Match 91.3%; Score 1391.2; DB 3; Length 1853;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 68; Indels - 2; Gaps 2;
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Qy 422 TCTGGCTCTACAAAGCAGCAGACACTGATGTTGCTGTTTCTCTTACTGACACCAACA 481
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Qy 1381 AACTCGTCTATAGATAACCTGCCGAGGAGGTGTTGCAAAATTCATATGSCCTCCAAAGG 1440
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Qy 1441 GAGCAGCAGGAGGAGCTTAAGAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTCAG 1500
Db 1510 GAGCAGCAGGAGGAGCTTAAGAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTCAG 1569
Qy 1501 CAGTCTCCGAGGAGGCTGTGGCTTAA 1524
Db 1570 CAGTCTCCGAGGAGGCTGTGGCTTAA 1593

RESULT 2

US-09-108-010B-13
Sequence 13, Application US/09108010B
Patent No. 6362399
GENERAL INFORMATION:
APPLICANT: ANTHONY JOHN KINNEY
INVENTOR: GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-108-010B-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;
Best Local Similarity 62.8%; Pred. No. 2.9e-139;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

Qy 5 AGCAACCGGAGGAGACGCGTGCAGTTCAGCGCTCAATGCGCAGAGACCTGACAAATC 64
Db 71 AGCAGCCACACCAAAACGAGTGCAGATCCACGCGCTCAATGCGCTAAAAACCGGATTAAC 130
Qy 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACCAACAGAGTTCGAAT 124
Db 131 GTATAGAGTCAGAGGTTGCTTCATTGAGACATGGAAACCCCTTAACAACAGCCATTCCAGT 190

QY 125 GCGCGGCGTCCCTCTCTGCGCTTAGTCTCTCCCGCGAAGCCGCTTCGTAGGCGTTTCT 184
Db 191 GTGCGGTGTGCGCTCTCTGCGTGCACCCCTTCAACCGCAACGCGCTTCGAGAGCTTCCT 250
QY 185 ACTCCAAATGCTCCCGAGGAGATCTTCAATCCAGCAAGGAGGATACCTTTGGGTGATAT 244
Db 251 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTGATGTTATTTTGGCATGATAT 310
QY 245 TCCTCGTGTCTCTAGACACTATGTAAGAGGCTCACACAAAGGTCTGATCTCAGTCCC 304
Db 311 TCCGCGGTCTCTAGCACATTTGAAGAGCT----- 342
QY 305 AAAGACCAACAGAGCTCTCAAGGAGAGAACCAAGCCAAACAGCAACGAGATAGTCAAC 364
Db 343 -----CAAAAAGAGCAAAAGCAGCAGCGCCCAAGAGCGTCAAC 382
QY 365 AGAAGGTGACCGTTTCGATGAGGCTGATCTCAATGCGAGTTCACCGGTTGCTTTCT 424
Db 383 AGAAGATCTATCACTTCAGAGAGGCTGATTTGATGCGAGTGCACCGGTTTGCATACT 442
QY 425 GGCTCTACAAACGACCACTGATGTTGCTGCTTTCTTCTTCTGACACCAACAACA 484
Db 443 GGATGTACAAATGAAGACACTCTGCTTCTGCGGTTCTTATTGACACCAACAGCT 502
QY 485 ACAGCAACAGCTTGATCTATCCCGAGGAGTTCATTTGGCTGGGAAACAGGAGCAAG 544
Db 503 TCAGAAACAGCTCGACAGAGCTAGGAGATCTATCTTGTGGGAAACCAAGAGCAAG 562
QY 545 AGTTCTTAGGTACCGACCAAGCAGACAGCAAGAGGCTTACCATATAGCC 604
Db 563 AGTTCTTAGGTACCGACCAAGCAGCAAG----- 595
QY 605 CATACAGCCGCAAAAGTCAGCTAGACAAAGAGCGTGAATTTAGCCCTCGAGGACAGC 664
Db 596 -----GAGGTACTC 604
QY 665 ACAGCGCAGAGAACGAGCAGGAGCAAGAAAGAAACGAAAGTGGAACATCTTCAGCG 724
Db 605 AAAGCAGAAAGAAAGCGTCAGCAAGAAAGAAAGAAAGAGGAGCGCAGCATATTCAGTG 664
QY 725 GCTTCAGCGGAGTTCTTGACCAAGCTTCCAGGTTGACGACAGACAGATAGTCAAA 784
Db 665 GCTTCGCGCGGAAATCTTGGAACATGCGGTC---GTGCTGGACAGGAGATAGTGAA 721
QY 785 ACCTAAGAGCGAGACGAGTGAAGAGAGGAGGCAATTTGACAGTGAAGGGAGGCG 844
Db 722 AGCTAAGGTGAGAGAGAGAGAGAGAGAGGTCATTTGACAGTGAAGAGGAGTC 781
QY 845 TCAGAAATCTTGAGCCAGATAGAAAGAGAGCGTCCGACGAGAGAGGAGATACGATGAAG 904
Db 782 TCAGCGTGATAGCCCAACCCAGCAAGAGCAGCAACAAAGACCGAGGAGAGGAGAGC 841
QY 905 ATGAATATGAATAGATGAAGAGATAGAGGCTGGCGGGGAAACGAGGAGGAGGGA 964
Db 842 CAGATTGTGACGAGAAAGCAACAT-----TCCCAAGGCCAAGCAGAA 886
QY 965 ATGGTATTGAAGAGAGATCTGACCGCAAGTGCTTAAAGACATTTGTTAGAAACAGAT 1024
Db 887 ATGGCAATGACGAGACATTTGACAAATGAGACTTCGCCACACATTTGCCAGACTTCAT 946
QY 1025 CCCTGACATCTCAACCCCTCAAGCTGGTTCACTCAAAAAGTGCACACGATCTCAACCTTC 1084
Db 947 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCACACCGCTACCGCTCGACTTC 1006
QY 1085 TAATACCTTAGGTGGCTTGGACCTAGTGTGAATATGGAATCTCTACAGAAATGCAATGTT 1144
Db 1007 CAGCCCTCTGTGGCTCAAACTCAGTGCAGGCTTGGATCACTCCGCAAGAAATGCTATGT 1066
QY 1145 TTGTGCTCACTACCAACCAACGACAGCATCATATATCGATTGAGGGAGCGGCTC 1204
Db 1067 TGTGCGCACACTACCAACCTGAAACGCAACAGCAATAATATACGCAATTAATGAGCGGCA 1126
QY 1205 ACGTGCAAGTCTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGTC 1264

Db 1127 TGCTACAAGTGGTGAATTTGCAATGGTGAGAGAGTGTGATGAGAGCTGCAAGAGGAC 1186
QY 1265 ACGTGCTTGTGGTGGCCACAGAACTTCGCGCTCGCTGCTGAAAGTCCAGAGCGAGAACTTCG 1324
Db 1187 AGGTGTTAAATTTGTGCCACAAAACCTTTGCGGTGGCTGCAAGATCACAGAGCGCAACTTCG 1246
QY 1325 AATACGTGGCATTTCAAGACAGACTCAAGGCCAGCATAGCAACCTCGCGGTGAAAAC 1384
Db 1247 AGTATGTTTCATTCAAGACCAATGATAGACCTCGATCGCAACCTTGCAAGTGCAAACT 1306
QY 1385 CGCTCATAGATAACCTTCGCGAGGAGGTGTTGCAAAATTCATATGGCTCCAAAGGAGC 1444
Db 1307 CATTTGTTGAACGATTCGCGAGGAGTGAATTCAGCAAACTTTTAACTTAAGGAGGAGC 1366
QY 1445 AGCAAGGAGCTTAAGAAACAAACCCCTTCAAGTTCCTGTTCCACCGCTCTCAGCAGT 1504
Db 1367 AGCCAGGAGGTCAAGAAACAAACCCCTTTCAGCTTCTGTTCCACCTTAAGAGTCTC 1426
QY 1505 CTCGAGGCGTGTGGCTTA 1523
Db 1427 AGAGGAGAGTTGTGGCTTA 1445

RESULT 3

US-09-758-652-13
; Sequence 13, Application US/09758652
; Patent No. 6703544
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14,1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-758-652-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;
Best Local Similarity 62.8%; Pred. No. 2.9e-139;

Matches	954;	Conservative	0;	Mismatches	421;	Indels	144;	Gaps	4;	
Qy	5	AGCAACCGGAGGAGAA	CGCGT	GCCAGTTC	CAGCGCCCTCA	ATGGCGCAGAGACCTGCA	CAATC	64		
Db	71	AGCAGCCACAGCAAA	ACGAGTGC	CAGATC	CAACGCCTCA	ATGCTTAAACCGGATA	CAAC	130		
Qy	65	GCATTGAATCAGAGGG	GGTTAC	ATTGAGACT	TTGGAACCCCA	CAACCCAGGAGTTCGA	AT	124		
Db	131	GTATAGAGTCAGAAG	TGGCTT	CATTGAGAC	ATGGAA	CCCTTAA	CAACAGGCCCATTC	CAAT	190	
Qy	125	GCGCGCGGTGCGCCT	CTCTCG	TTAGTCT	CCGCGCAAC	CGCCCTTCGT	PAGCCTTTCT	184		
Db	191	GTGCGGGTGTGCGCT	CTCTCG	CTGACCT	CAACCGCA	CGCCCTTCG	CAGACCTTCT	250		
Qy	185	ACTCCAAATGTCGCC	AGGAGAT	CTTCAT	CAGCAAG	GAAGGGAT	ACTTTGGTGTG	ATAT	244	
Db	251	ACAACCAACGCTCC	CCAGGAGAT	CTACAT	CAACAA	AGGTAGT	GGTATTTTTGGCAT	ATAT	310	
Qy	245	TCCTGGTTCCTAG	ACACTAT	GAAGAG	CGCTCAC	ACAAAGT	CGTCGATCT	CAGTCCC	304	
Db	311	TCCCGGGTGTCT	AGACAT	TTGA	AGAGCT	-----	-----	342		
Qy	305	AAAGACCAAC	AGAAGCT	CTCA	AGGAGAA	GAACAA	AGCCAA	ACGAGAT	AGTCA	364
Db	343	-----	-----	-----	-----	-----	-----	-----	382	
Qy	365	AGAAAGTGAC	CGTTTC	GATGAG	GGTGAT	CTCAT	TTGCAG	TTCCAC	CGGTGTT	424
Db	383	AGAAGATCTAT	CACTTC	CAGAGAG	GGTGA	TTGAT	TGCAGT	GCCAA	CGGTTTT	442
Qy	425	GGCTCTACA	ACGAC	CGACACT	GTATG	TTGTTCT	CTTCTT	ACTG	CACCA	484
Db	443	GGATGTACA	CAATGA	AGACACT	CTCTG	TTGTTGCC	TTTCTT	ATTG	CACCA	502
Qy	485	ACGACAA	CCAGCT	TGATCAG	TTCC	AGGAGAT	TCAAT	TTTGG	CTGGAA	544
Db	503	TCAGAA	CCAGCT	CGACCA	TGCTAG	GAGATTT	CTATCT	TTG	CTGGAA	562
Qy	545	AGTTCTTAA	GGTAC	CGCAAC	AAAGC	AGACAG	CAACG	AGTCTT	ACCATAT	604
Db	563	AGTTCTTAC	AGTAT	TCGCC	ACAG	AGCAG	CAAG	-----	-----	595
Qy	605	CATAC	CGCCG	CAAAAGT	CAGCCT	TAGACA	GAAGCG	TGAAT	TTAGCCCT	664
Db	596	-----	-----	-----	-----	-----	-----	-----	-----	604
Qy	665	ACAGCCG	CAGAAC	GACG	AGGACA	GAAGAA	AGGAAG	GTGG	AAACATCTT	724
Db	605	AAAGCC	AGAAAG	GAAGCG	TGAC	GAAGAA	GAAGAA	ACGA	AGAGG	664
Qy	725	GCTT	CAGCCGG	AGTTCT	CTGGA	CAAG	CCCTTCC	AGGTTG	ACGACAC	784
Db	665	GCTTC	CGCCCG	GAATCT	TTGGA	CAT	CGCTC	---G	TCGTGG	721
Qy	785	ACCTA	AGAGCG	AGACCG	GAGTGA	AGAGAG	GCGCAT	TTGTGA	CHAGT	844
Db	722	AGCTA	CAAGGT	GAAGCA	AGAGAG	AGAGGG	TGCCAT	TTGTCA	CACTG	781
Qy	845	TCAGA	ATCTTT	GAGCC	CAGATAGA	AAAGAG	CGTGC	CGCAG	AAAGAG	904
Db	782	TCAG	CGTGAT	AA	CGCCAC	CCGAG	AGAG	AGCA	AAAGAC	841
Qy	905	ATGA	ATATGA	ATAC	GATGA	AGAGAT	AGAG	CGGTGG	CAGGG	964
Db	842	CAG	ATTGT	GACGA	AAAGACA	AAAT	-----	-----	-----	886
Qy	965	ATG	GTATT	GAAG	AGAC	CAATCT	GAC	CCAGT	GCTTAA	1024
Db	887	ATG	CGATT	GACGA	AGAC	CAATTT	GACAA	ATG	AGACTTT	946
Qy	1025	CCC	CTG	ACAT	CTTA	CAAC	CCCTCA	AGCTGG	TTTCACT	1084
Db	947	CAC	CTG	ACAT	CTTCA	AC	CCCTCA	AGCTGG	TAGATCA	1006

RESULT 4

US-10-684-651-13
; Sequence 13, Application US/10684651
; Patent No. 6828491
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/684,651
; FILING DATE: 14-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14,1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1446 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-684-651-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;

Best Local Similarity 62.8%; Pred. No. 2.9e-139;

Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

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Qy 5 AGCAACCGGAGGAAACGCGTCCAGCTTCCAGCCCTCAATGCGCAGAGACCTGACAAATC 64
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 71 AGCAGCCACAGCAAAACGAGTGCCAGATCCAAACGCTCAATGCCCTAAACCGGATAC 130
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 65 GCATTGAATCAGAGGCGGTTCATTGAGACTTGGAAACCCCAACCAACAGAGGTTGCAAT 124
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 131 GTATAGAGTCAGAAGGTGGCTTCATTGAGACATGGAACCCCTTAACAACAAGCCATTCCAGT 190
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 125 GCGCCGGCTGCGCTCTCTCGCTTAGTCTCCGCCCAAGCCCTTCGTAGGCTTTCT 184
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 191 GTGCCGGTGTGCCCTCTCTCGCTGCACCTCAACCCGCAACGCCCTTCGAGAGCTTCCT 250
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 185 ACTCCAAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTGATAT 244
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 251 ACACCAAGCTTCCCGAGGAGATCTACATCCAAACAGGTAGTGTATTTTGGCATGATAT 310
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 245 TCCTCGTGTCTCTGATGACATTAAGAGAGCTTCAACACAAAGGTCTCTAGTCC 304
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 311 TCCGGGTGTCTCTAGCACATTTGAAGAGCT----- 342
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 AAAGACCAACAGACGTCTCCAGGAGAAACCAACCAAGCAACAGCAAGATAGTCACC 364
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 343 -----CAACAAAGAGCAACAGCAGCGCCCAAGACCGTCACC 382
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 365 AGAAGGTGACCGTTTCGATGAGGTGATCTCATTCAGTTCCTCCACCGGTGTTGCTTCT 424
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 383 AGAAGATCTATCTTCAGAGAGGTGATTTGATTCAGTTCGCAACCGGTTTTCATCT 442
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 425 GGCTCTAACACGACCACTGATGTTGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 484
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 443 GGATGTACAACAATGAAGACACTCTCTGTTGTCGCTTCTTCTTCTTCTTCTTCTTCTTCT 502
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 485 ACACACACAGCTTGATCAGTTCCTCCAGGAGATCAATTTGGCTGGGAACACGAGCAAG 544
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 503 TCCAGAACAGCTCGACAGATGCTTAGGAGATTTCTATCTTGTCTGGGAACCAAGACCAAG 562
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 545 AGTTCTTAAGGTACCAACAAAGCAGACAAAGCAGACGAAAGGCTTACCATATAGCC 604
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 563 AGTTCTTAAGGTACCAACAAAGCAGACAAAGCAGACGAAAGGCTTACCATATAGCC 595
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 605 CATACAGCCCGCAAGTTCAGCTTAGAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC 664
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 596 -----GAGGTACTC 604
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 665 ACAGCCGACAGAACGAGCAGGACGAGCAAGAAAGCAAGAGGTGGAAACATCTTCAGCG 724
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 605 AAAGCCAGAAAGGAAGCGTCAGCAAGAAAGAAACGAAAGGAGGAGGAGCATATTCAGTG 664
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 725 GCTTCAGCCGGATTCCTCGAAACAGCTTCCAGGTTGACGACAGACATAGTCAAA 784
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 665 GCTTCGCCCCGAAATTTTGAACATCGCTTC---GTCGTGACAGGACAGATAGTGAA 721
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 785 ACCTAAGAGCGAGACCGGAGGTGAAGAGAGGAGGACATTTGACAGTGAAGGAGGCGCC 844
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 722 AGCTACAGGTGAGAACGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 781
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 845 TCAGAAATCTTTAGCCCAAGATAGAAAGAGAGAGGTCGCGGACGAGAGAGGAATACGATGAG 904
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 782 TCAGCGTGATAAGCCCAACCCAGAGAGAGCAACAAAGACCCGAGGAGAGAGAGAGAGAGC 841
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 905 ATGAATATGAATACGATGAAGAGGATAGAAGGCGTGGCAGGGGAAGCAGAGCGAGGGGA 964
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 842 CAGATTGTCAGGAAAGACAAACAT-----TGCCAAAGCCCAAGCAGAA 886
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 965 ATGTTATGAAGAGACGATCTGCACCCCAAGTGCTAAAAGAACATTGGTTAGAAACAGAT 1024
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 887 ATGTCATTGACGAGACCAATTTGCACAATGAGACTTCGCCCAACAACTTGGCCAGACTTTCAT 946
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1025 CCCTGACATCTACAACCCCTCAAGCTGTTTCACTCAAAACTGCCAAAGATCTCAACCTTC 1084
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 947 CACTGACATCTTCAACCCCTCAAGCTGGTAGCATCACACCGCTACCAGCCTCGACTTCC 1006
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1085 TAATACTTAGTGGCTTGGACCTAGTCTGTAATATGAAATCTCTACAGGAATGCATTGT 1144
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1007 CAGCCCTCTCTGCTCAAACTCAGTGCCTCAGTTTGGATCCTCCGCAAGAAATGCTATGT 1066
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1145 TTGTGCTCTACTACAACCAACGACACAGCATCATATATTCGATTGAGGGGAGCGGCTC 1204
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1067 TCGTGCACACTACAACCTGAACGCAACAGCATATATACGCAATTGAATGGACGGGCAT 1126
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1205 ACGTGAAGTCGTGGACAGCAACGCAACAGAGTGTACGACGAGAGCTTCAAGAGGCTC 1264
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1127 TGGTACAAGTGGTGAATTTGCAATGGTGAAGAGTGTGATGGAGAGCTGCAAGAGGGAC 1186
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1265 ACGTGTCTTGTGGTCCCAAGAACTTCCCGCTCGCTGGAAAGTCCAGAGCGAGAACTTCG 1324
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1187 AGGTGTTAATTTGGTCCCAAACTTTGCGGTGGCTGCAAGATCACAGAGCACAACCTTCG 1246
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1325 AATACGTGGCATTAAGACAGACTCAAGGCCAGCAGATAGCAACCTCGCGGTGAAAAC 1384
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1247 AGTATGTTTCAATCAAGACCAATGATAGACCTCGATCGGCAACCTTGCAGGTGCAAACT 1306
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1385 CCTCATAGATACTCGCGGAGAGTGGTTCGAATTCATATGCGCTCCAAAGGGAGC 1444
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1307 CATTTGTAACGCAATTCGCGGAGAGTGAATCAGCAAACTTTTAACTAAGAGGGCAGC 1366
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1445 AGCAAGGAGCTTAAGAAACAAACCCCTTCAAGTTCTTTCGTTCCACCGCTCTCAGCAGT 1504
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1367 AGCCAGGAGCTCAAGAACAAACCCCTTTCAGCTTCTGTTCCACCTTCAAGAGTCTC 1426
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1505 CTCGAGGGCTGTGGCTTA 1523
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1427 AGAGGAGTGTGGCTTA 1445
Dy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 5

US-09-108-010B-11

; Sequence 11, Application US/09108010B

; Patent No. 6362399

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; APPLICANT: GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/108,010B

; FILING DATE: 30-Jun-1998

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-108-0108-11

Query Match 33.7%; Score 513; DB 3; Length 1488;
Best Local Similarity 62.7%; Pred. No. 5.Se-138;
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;
QY 5 AGCAACGGGAGGAGACGGGTGCGCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC 64
DB 71 AGCAGCCTCAGCAAAACGAGTGCAGATCCAAAACCTCAATGCGCCTCAAAACCGGATAACC 130
QY 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACAAACAGGAGTTCGAAT 124
DB 131 GTATAGATCAGAGGAGGGCTCATTTGAGACATGGAACCTCAACAAACAGCCATTCCAGT 190
QY 125 GCGCCGGGTGCGCCTCTCTCGTCTAGTCTCCGCGCGCAAGCCCTTCGTAGCCCTTTCT 184
DB 191 GTCCGGTGTGTCCTCTCTCGTGCACCTCAACCGCAACGCGCTTCGTAGACCTTTCT 250
QY 185 ACTCCATGTCCTCCAGGAGATCTTCATCCAGCAAGGAGGGGATACTTTGGGTGATAT 244
DB 251 ACACCAACGGTCCCAAGGAATCTATCCAAACAGTAAGGTATTTTGGCATGATAT 310
QY 245 TCCTCTGTTGCTTAGACACTATGAAGAGCCTCACACACAAGGTCGTGCGATCTCAGTCCC 304
DB 311 ACCCGGGTGTCTAGACACTTTGAAGAGCCTCA----- 344
QY 305 AAAGACCAACAGAGCTTCCAGGAGAGAGACCAAGCCCAACAGCAACGAGATAGTCAAC 364
DB 345 -----ACAACCTCAACAAAGAGGACAAAGCAGCAGACCAACAGACCGTCAAC 391
QY 365 AGAAGGTGCAACCGTTCGATGAGGCTGATCTCAATGCGCTCCACCGGTGTTGCTTTCT 424
DB 392 AGAAGATCTATACTTCAGAGAGGGTATTTGATCGCAGTGCCTACTGTTGTTGCAATGTT 451
QY 425 GGCTCTACACAGCACCAGCACTGATGTTGCTGTTCTTTACTGACACCAACAACA 484
DB 452 GGATGTACAACATGAAGACACTCTCTGTTGTCGGCTTCTATTATGACACCAACAGCT 511
QY 485 ACACAAACAGCTGTGATGATTCCTCCAGGAGATTCATTTGGCTGGGAACACCGAGCAAG 544
DB 512 TGGAGAACCAGCTCGACAGATGCTAGGAGATTTCTATCTTGTGGGAACCAAGAGCAAG 571
QY 545 AGTTCTTAAGGTACCAACAGCAGACAAAGCAGACAAAGCAGCAGCAAGCTTACCATATAGCC 604
DB 572 AGTTCTTAATATCAGCAAG----- 594
QY 605 CATAACGCGCAAAAGTTCAGCCTAGACAAAGAGCGTGAATTTAGCCCTCGAGGACAGC 664
DB 595 -----CAAGGAGGTCAATC 607
QY 665 ACAGCCGACAGAGACGAGGAGGACAGAAAGAAACGAGGTGGAACATCTTCAGCG 724
DB 608 AAAGCCAGAAAGAAAGCATCAGCAAGAAAGAAACGAAAGGAGCGGACATATTGAGTG 667
QY 725 GCTTCAGCGGGAGTTCTCGAACAAGCCTTCAGGTTGACGACAGACAGATAGTGCAAA 784

DB 668 GCTTCAACCTCGAAATTTCTTGGAACTGCAATTCAGCGT---GGACAAGCAGATAGCGGAAA 724
QY 785 ACCTAAGAGCGAGACCGAGAGTGAAGAAGAGGGAGCCATTGTGACAGTGTAGGGGAGGCC 844
DB 725 ACCTAAGAGGAGAGAACGAAGGGGAGAGCAAGAGGAGCCATTGTGACAGTGAAGAGGAGTC 784
QY 845 TCAGAACTTTGAGCCCA-----GATAGAAAGAGAGAGTGTCCGACGAGAGAGGAAT 895
DB 785 TGAGCGTGATAAAACCCACCGGACGAGCAGCAAAAGACCCAGGAAAGAGAGAGAGAG 844
QY 896 AGCATGAAGATGAATA-----TGAATACGATGAAGAGGATAGAAGCGGTG 940
DB 845 AAGAGAGGATGAGAAGCCACAGTGCAGAGGTAAAGACAAACACTGCCAACGCCCGAG 904
QY 941 GCAGGGGAAGCAGAGGAGCGGGGAATGTTATGAAGAGAGGATCTGACCGCGAGTGCTA 1000
DB 905 GAAGCCAAAGCAAAAGCAGAGAAATGGCAATTTGACGAGACCATATGACCATGAGACTTC 964
QY 1001 AAAAGAACATTTGTAGAAAACAGATCCCTGACATCTACAAACCTCAAGCTGGTTCACTCA 1060
DB 965 GCCAACACATTTGCCAGACTTTCATCACCTGACATCTACAAACCTCAAGCGGTAGCGTCA 1024
QY 1061 AAACCTGCCAACGATCTCAACCTTTCTAATATCTTAGTGGCTTGGACCTAGTGTGAATATG 1120
DB 1025 CAACCGCCACAGCCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGCTGTTG 1084
QY 1121 GAAATCTTACAGGAATGCAATTTGTTGCTCCTACTACAAACCAAGCAGCAGCATCA 1180
DB 1085 GATCTCTCCGCAAGATGCAATTTGCTGCCACACTACAACTGAAACGCGAAACAGCATAA 1144
QY 1181 TATATCGATTGAGGGAGCGGCTCAGTGCAGTCTGTCGACAGCAACGCAACAGAGTGT 1240
DB 1145 TATACCATTTGAATGACGGGCATTTGATACAGTGTGTAATTCACACGGTGAGAGTGT 1204
QY 1241 ACACGAGGAGCTTCAAGAGGGTCACTGCTGTTGTTGCCACAGAACTTCGCCGTGCTG 1300
DB 1205 TTGATGAGAGCTGCAAGAGGGACGGTGTGATCTGTCACAAAACCTTTGTGGTGGCTG 1264
QY 1301 GAAAGTCCAGAGCAGAGAACTTCGAATACGTGCAATTCAGACAGACTCAAGGCCAGCA 1360
DB 1265 CAAGATCAGAGTGAACACTTCGAGTATGTGTCATTCAAGACCAATGATACACCATGA 1324
QY 1361 TAGCACAACCTCGCGGTGAAACCTCCGTATAGATAAACCTGCGGAGGAGTGGTTGCAA 1420
DB 1325 TCGGCACTTTGACGGGCAAACTCATTTGTAACGCAATTACCAGAGAGTGTATTTCAGC 1384
QY 1421 ATTATATATGCGCTTCCAAAGGGAGCAGGCAAGGAGCTTAAAGAAACAACACCCCTTCAAGT 1480
DB 1385 ACACCTTCAACCTAAAAGGCCAGCAGGCGAGATAAAGAAACAACACCCCTTCAAGT 1444
QY 1481 TCTTCGTTCCAGCTCTCAGCAGTCTCCGAGGGCTGTGGCTTA 1523
DB 1445 TCCTGGTTCCACCTCAGGAGTCTCAGAAGAGAGCTGTGGCTTA 1487

RESULT 6
US-09-758-652-11
; Sequence 11, Application US/09758652
; Patent No. 6703544
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; ; GARY MICHAEL FADER
; ;
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; ; CLASSES OF SOYBEAN SEED
; ; PROTEIN GENES
; ;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
;

ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNN M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-758-652-11

Query Match 33.7%; Score 513; DB 3; Length 1488;
Best Local Similarity 62.7%; Pred. No. 5.5e-138;
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;

QY 5 AGCAACCGGAGGAAACGCTGTCAGTCCAGCGCTCAATGCCAGAGACCTGACAAATC 64
DB 71 AGAGCCCTCAGCAAAACGAGTGGCCAGATCAAAACCTCAATGGCCCTCAACCCGGATAAC 130
QY 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACAAACAGGAGTTGCAAT 124
DB 131 GTATAGATCAGAAGGAGGCTCATTTGAGACATGGAACCTTAACAAACAGCCATTCCAGT 190
QY 125 GCGCGGCGTGCCTCTCTCGCTTAGTCTTCGCGCGCAACGCCCTTCGTAGGCGCTTCT 184
DB 191 GTCCCGGTGTGCGCTCTCTCGCTGACCCCTCAACCGCAACGCCCTTCGTAGACCTTCCT 250
QY 185 ACTCCAAATGCTCCCGAGGATCTTCATCCAGCAAGAGGGGATCTTTGGGTGATAT 244
DB 251 ACACCAACCGTCCCGAGGAAATCTACATCCAAAGGTAAAGGTATTTTGGCATGATAT 310
QY 245 TCCTCGTTGCTTAGACACTATGAAGAGCTTCACACAAAGGTGCTGATCTCAGTCCC 304
DB 311 ACCCGGTGTCTAGACACTTTGAAGAGCTCA----- 344
QY 305 AAAGACCAACAGAGCTTCAAGGAGAGAGCAACCAAGCCCAACAGACAGATAGTCACC 364
DB 345 -----ACAACCTCAACAAAGAGGACAAAGCAGCAGACACCAAGACCGTCACC 391
QY 365 AGAAGGTGACCGTTTCGATGAGGTGATCTCATTGCGATTCCTCCACCGGTGTTGCTTCT 424
DB 392 AGAAGATCTATACTTCAGAGAGGGGTGATTGATCGCAGTGCCTACTGTTGGCATGGT 451
QY 425 GGTCTACAAACGACCAACGACACTGATGTTGCTGTTTCTTCTTACTGACACCAACAAACA 484
DB 452 GGATGTACACATGAAGACACTCTCTGTTGTCGCTTCTATATTTGACACCAACAGCT 511
QY 485 ACACCAACAGCTTGATCAGTCCCGAGGAGATTCAATTTGGCTGGGAACACCGGCAAG 544
DB 512 TGGAGAACCAAGCTCGACAGATGCTTAGGAGATTCTATCTTCTGCTGGGAACCAAGCAAG 571
QY 545 AGTTCTTAAGTACCAGCAACAAAGCAGACAAAGCAGACGAAAGCTTACCATATAGCC 604
DB 572 AGTTCTTAATAATATCAGCAAGAG----- 594

RESULT 7

US-10-684-651-11
; Sequence 11, Application US/10684651
; Patent No. 6828491
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER

QY 605 CATAACGCGCAAAAGTCAGCTAGACAGAGAGCGTGAATTTTAGCCCTCGAGGACAGC 664
DB 595 -----CAAGGAGGTATC 607
QY 665 ACAGCCGAGAGAACGAGAGGACAGAGAAAGAAACGAGAGGTGGAAACATCTTTCAGCG 724
DB 608 AAAGCCAGAAAGGAAAGCATCAGCAAGAAAGAAACGAGAGGAGGAGCATATTTAGTGT 667
QY 725 GCTTCAGCGCGGAGTTCCTGGAACAAGCCCTCCAGGTTGACGACAGACAGATAGTGAAA 784
DB 668 GCTTCACCTTGAATTTCTGGAACATGCTTCAGCGT-----GGACAGACAGATAGCGAAA 724
QY 785 ACCTAAGAGCGGAGACCGAGAGTGAAGAGAGGAGGACCATTTGTGACAGTGAAGGAGGCC 844
DB 725 ACCTAAGAGGAGAGAACGAGAGGAGGAGCAACAGGAGGCCATTTGTGACAGTGAAGGAGGTC 784
QY 845 TCAGAAATCTTTGAGCCCA-----GATAGAAGAGACGTGCCGACGAGAAAGAGGAAT 895
DB 785 TGAGCGGTGATAAAACCCACCGACGAGCAGCAACAAAGACCCCGAGAAAGAGGAAG 844
QY 896 ACGATGAAGATGAATA-----TGAATACGATGAAGAGGATAGAGAGCGGTG 940
DB 845 AAGAAGAGGATGAAGAGCCACAGTGCAGGGTAAAGACAAACCTGCTCAACGCCCGAG 904
QY 941 GCAGGGGAGCAGAGGCGGGGAAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTGCTA 1000
DB 905 GAAGCCAAAGCAAAAGCAGAGAAATGGCATTCAGGAGACCATATGCACCATGAGACTTC 964
QY 1001 AAAAGAACATTGGTAGAAACAGATCCCTTCACATCTACAAACCTCAAGCTGGTTCACTCA 1060
DB 965 GCACAAACATTTGCCAGACTTCATCACCTGACATCTACAAACCTCAAGCGCGTAGCGTCA 1024
QY 1061 AAATGCGCAACGATCTCAACCTTCTAATCTAGTGGCTTGGACCTAGTGTGCTGAATATG 1120
DB 1025 CAACCGCCACGACCTTGACTTCCAGCCCTCTGCTGGCTCAGACTCAGTGTGCTGAGTTG 1084
QY 1121 GAAATCTCTACAGGAATGCAATTTGTCGCTCACTACACACCAACGACACAGCATCA 1180
DB 1085 GATCTCTCCGCAAGAATGCAATGTTCTGTCACACTACAACTGAAACGCGAACAGCATAA 1144
QY 1181 TATATGATGAGGGAGCGGCTCAGTGCAGTCTGAGACAGCAACGCGCAACAGAGTGT 1240
DB 1145 TATACGATTTGAATGGACGGGCAATTGATACAAAGTGGTGAATTCACACGCTGAGAGAGTGT 1204
QY 1241 ACCACGAGAGCTTCAAGAGGGTCAGTGTCTGCTGGTGCACAGAACTTCGCGCTGCTG 1300
DB 1205 TTGATGAGAGCTGCAAGAGGGACGGGTGCTGATCGTGCACAAACCTTTGTGTGCTG 1264
QY 1301 GAAAGTCCAGAGCGAGAACTTCGAATACGTGGCATTTCAAGACAGACTCAAGGCCAGCA 1360
DB 1265 CAAGATCAGAGTGACAACTTCGAGTATGTGTTCATTCAAGACCAATGATACACCCATGA 1324
QY 1361 TAGCCAACTTCGCGGTGAAACTCCGTCATAGATAACCTGCGGAGGAGGTGGTTGCCAA 1420
DB 1325 TCGGCACTCTTTCAGGGGCAAACTCATTTGTAACGCTATTACAGAGGAAGTATTTCAGC 1384
QY 1421 ATTATATGGCTTCAAGAGGAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1480
DB 1385 ACATTTCAACCTTAAAGAGCCAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1444
QY 1481 TCTTCGTTCCACCGCTCTCAGAGCTCTCCGAGGGCTGTGGCTTA 1523
DB 1445 TCCTGTTCCACCTCAGGAGTCTCAGAGAGAGCTGTGGCTTA 1487

TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996

ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-684-651-11

Query Match 33.7%; Score 513; DB 3; Length 1488;
Best Local Similarity 62.7%; Pred. No. 5.5e-138;
Matches 968; Conservative 0; Mismatches 425; Indels 150; Gaps 5;

QY	5	AGCAACCGGAGGAGAACGCTGCGAGTTCCAGCGCCTCAATGCGCAGAGACCTGACAATC	64
DB	71	AGCAGCCTCAGCAAAACGAGTGCAGATCCAAAACCTCAATGCGCTCAAAACCGATAACC	130
QY	65	GCATTGAATCAGAGGGCGGTTCATTGAGACTTGGAAACCCCAACACCCAGGAGTTGGAAT	124
DB	131	GTATAGAGTCAGAAGGAGGCTCATTGAGACATGGAACCCCTAAACAAGCCATTCCAGT	190
QY	125	GCGCCGGCTGCGCCTCTCTCGTTAGTCTCCGCCCAAGCCCTTCGTAGGCGCTTCT	184
DB	191	GTGCCGGTGTGCGCCTCTCTCGTGCACCCCTCAACCGCAACGCCCTTCGTAGACCTTCCT	250
QY	185	ACTCCCAATGTCGCCAGGAGATCTTCATCCAGCAAGGAAGGGGATACCTTTGGGTGATAT	244
DB	251	ACACCAACGTTCCCGAGGAATCTACATCCNACAGGTAAAGGTATTTTGGCATGATAT	310
QY	245	TCCTCGTGTGCTCTAGACATATGAAGAGCTCTACACAAAGGTGCTCGATCTCAGTCCC	304
DB	311	ACCGGGTGTGCTCTAGCACATTTGAAGAGCCTCA-----	344
QY	305	AAAGACCACCAAGACGCTCCNAGGAGAAGCAAGCCCAACAGCAACAGAGATAGTCACC	364
DB	345	-----ACAACTCAACAAAGAGGACAAGAGGACAAGAGCGACCAAGACCGTCACC	391
QY	365	AGAAGTGACCGGTTTCGATGAGGGGTGATCTCATTTGCAAGTTCCCAACCGGTTGCTTCT	424
DB	392	AGAGATCTATACTTCAGAGAGGGTGTGATTTGATCGCAGTGCCTTACTGTTGGTTCATGGT	451

QY	425	GGCTCTACAAACGACACGACACTGATGTTGTTGCTGTTTCTTCTACTGACACCAACA	484
DB	452	GGATGTACAAACAATGAAGACACTCTCTGTTGTTGCGCTTTCTATTATGACACCAACAGCT	511
QY	485	ACGACAAACAGCTTGTATCAGTTCCCGCAGGAGATTCAATTTGGCTGGAAACACCGAGCAAG	544
DB	512	TGGAGAACAGCTCGACAGATGCTTAGAGATTCTTATCTTGTGGGAACCAAGAGCAG	571
QY	545	AGTTCTTAAGGTACACGACCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATATAGCC	604
DB	572	AGTTTCTAAAATATACGAAGAG-----	594
QY	605	CATACAGCCCGCAAGTCAAGCTAGACACAGAAGAGCGTGAATTTAGCCCTCGAGGACAGC	664
DB	595	-----	607
QY	665	ACAGCCGACAGAGAAACGAGCAGGACGAAGAAGAAACGAAGGTGGAACATCTTCAGCG	724
DB	608	AAAGCCAGAAAGGAAGCATCAGCAAGAGAGAGAAACGAGGAGCAGCATATTGAGTG	667
QY	725	GCTTCAAGCGGAGTTCTTGGAAACAAAGCCTTCCAGGTTGACGACAGACAGATAGTCAAA	784
DB	668	GCTTCAAGCGGAGTTCTTGGAAACATGCAATTCAGCGT---GGACAAGCAGATAGCGAAA	724
QY	785	ACCTAAGAGCGAGACGAGAGTGAAGAAGAGGAGGCCATTGTGACAGTGAAGGGAGGCC	844
DB	725	ACCTAAGAGGAGAGAACGAAGGGAAGACAAGGGAGCCATTGTGACAGTGAAGGGAGGTC	784
QY	845	TCAGAAATCTTGAGCCCA-----GATAGAAAGAGAGCGTCCGACGACGAAGAGAGGAAT	895
DB	785	TGAGCGTGATAAACCAACCCACCGAGCAGCAGCAACAAGAGACCCAGGAAGAGAGAAAG	844
QY	896	ACGATCAAGATGAATA-----TGAAATCAGATGAAGAGGATAGAAGGGCTG	940
DB	845	AGAAGAGGATGAGAAGCCACAGTGCAGAGGTTAAAGACAAACACTGCCAACCGCCCCGAG	904
QY	941	GCAGGGAGACGAGGAGCGGGAATGGTATTGAAGAGAGATCTGCACCAGCAAGTGCTA	1000
DB	905	GAAGCCAAAGCAAAAGCAAGAAATGGCAATTCAGCAGAGCATTGACCATGAGACTTC	964
QY	1001	AAAAGAACATTTGGTAGAAAACAGATCCCTGACATCTACAACCCCTCAAGCTGGTTCACTCA	1060
DB	965	GCACAAACATTTGCCAGACTTCATCACTGACATCTACAACCCCTCAAGCGCGTAGCTCA	1024
QY	1061	AACTGCAACAGATCTCAACCTTCTTAATCTAGTGGCTTGACACTAGTCTGAATATG	1120
DB	1025	CAACCGCCACACGCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGAGTTG	1084
QY	1121	GAATCTCTACAGGAATGCAATTTGTTGCTCACTACAACCAACCAACGACACAGCATCA	1180
DB	1085	GATCTCTCCCAAGAAATGCAATGTTGTCGCACTACTACAACCTGNAAGCGCAACAGCATAA	1144
QY	1181	TATATCGATTGAGGGGACGGGCTCAGCTGCAAGTCTGTGGAAGCAACGCAACAGAGTGT	1240
DB	1145	TATACGATTTGAATGGACGGGCATTGATACAAGTGGTGAATTCGAACGGTGAGAGAGTGT	1204
QY	1241	ACAGAGGAGCTTCAAGAGGTCACGTGTTGTTGTCGACAGAACTTCGCGTCCGCTG	1300
DB	1205	TTGATGAGAGAGCTGCAAGAGGGGACGGGTGCTGATCGTGCACCAAACTTTGTGTGGCTG	1264
QY	1301	GAAGTCCCAAGAGCGAGAACTTCGAATACGTGGCATTCAGACAGAGCTCAAGGCCCCAGCA	1360
DB	1265	CAAGATCACAGAGTGCAACTTCGAGTATGTGTCATTCAGAGCAATGATACACCATGA	1324
QY	1361	TAGCCAACTTCGCGGTGAAAACTCCGTCAATAGATAACCTGCGGAGGAGGTGTTGCA	1420
DB	1325	TCGCACTCTTCAGGGGCAAACTCATTTGTTGAACGCATTACAGAGAGAGTGAATTCAGC	1384
QY	1421	ATTCAATGCGCTCCAAAGGGAGCAGGAGGAGCTTAAGAACAAACACCCCTTCAAGT	1480
DB	1385	ACACTTTCAACCTTAAAGAACGACGAGCCAGGCGAGATAAGAAACAAACCTTTCAAGT	1444


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; APPLICANT: Kinney, Anthony
; TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
; FILE REFERENCES: BB1432 US NA
; CURRENT APPLICATION NUMBER: US/09/805,694B
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,823
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Glycine max
US-09-805-694B-15

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Query Match 33.1%; Score 505; DB 3; Length 1746;

Query Match 33.1%; Score 303; DB 3;
Best Local Similarity 62.4%; Pred. No. 1.2e-135;

Best local similarity	92.4%	Freq. no.	1-28-133,
Matches	963;	Mismatches	430;
	Conservative	Indels	150; Gaps
	0;	Gaps	5;

[illegible]

RESULT 10

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US-09-108-010B-12
; Sequence 12, Application US/09108010B
; Patent No. 6362399
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; APPLICANT: GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95

```

SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,010B
FILING DATE: 30-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-108-010B-12

Query Match 33.1%; Score 504; DB 3; Length 1458;
Best Local Similarity 62.0%; Pred. No. 2,2e-135;
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;

QY 5 AGCAACGGAGGAGAACGCGTGCAGTTCAGCGCCCTCAATGCGCAGAGACCTGCAATC 64
DB 62 AGCAGGCACAGCAAAATGATGCGCAGATCAAAAGCTGAATGCCCTCAAAACCGGATAACC 121
QY 65 GCATTGAATCAGAGGGCGGTTACATTGAGATGGAACCCCAACACCGAGGAGTTCGAAT 124
DB 122 GTATAGATCGGAAGGTGGGTTCAATGAGACATGGAACCCCTAACAACAGCCATTCCAGT 181
QY 125 GCCTCCGGCTGCGCCCTCTCTCGCTTAGTCTCCGCGCCCAACGCCCTTCGTAGGCCCTTTCT 184
DB 182 GTCCCGGTGTGCGCCCTCTCTCGTCGACCCCTTAACCGCAATGCCCTTCGTAGACCTTCT 241
QY 185 ACTCCAAATGCTCCCGAGGAGATCTTCAATCCAGAAAGAGGGGATATCTTTGGTTGATAT 244
DB 242 ACACCAACGGTCCCGAGGAATCTACATACAAAGGTAATGTTATTTTGGCATGATAT 301
QY 245 TCCTCGTTGCTAGACACTATGAGAGCCTCACACAAAGTCTGTCGATCTCAGTCCC 304
DB 302 TCCCGGGTGTCTAGACCTTATCAAGAGCGCA----- 335
QY 305 AAAGACCAACAGACGTCTCCAGGAGAGAGACCAAAAGCCAAACAGACGAGATAGTCACC 364
DB 336 -----AGATCTCAGCAACGAGGAGAGAGCCCAAGAGCCCAAGACCGTCACC 382
QY 365 AGAAGTGCAACGTTTCGATGAGGGTGATCTATGAGTTCCTCCACCGGTGTTGCTTTCT 424
DB 383 AAAAGGTATACATCGCTTCAGAGAGGGTGATTTGATCGCAGTGCCTACTGCTGGTTGCAATGT 442
QY 425 GGCTCTACACGACACGACACTGATGTTGCTGTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 484
DB 443 GGATGTACACAAATGAAGACACTCCTGTTGTTGCGCGTTTCTATTATTGACACCAACAGCT 502
QY 485 ACACCAACACAGCTTGATCAGTTCCTCCAGGAGATTCAATTTGGCTGGGAACACCGGCAAG 544
DB 503 TGGAGAACACAGCTCGACAGATGCTTAGGATGTTCTATCTTGTGGGAACCAAGACCAAG 562
QY 545 AGTTCTTAAGGTACAGCAACAAAGACGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
DB 563 AGTTCTTAAGGTACAGCAACAAAGACGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 585
QY 605 CATAACGCGCCAAAGTCAAGCCTAGACAAAGAGCGGTGAATTTAGCCCTCGAGGACGC 664
DB 586 -----CAGCAAGGAGGTT 598

665 ACAGCCGAGAGAACGAGCAGGACGACAAAGAAAGAAACGAGGTGGAACATCTTCAGCG 724
DB 599 CCCAAAGCCAGAAAGGAAAGCAACAAAGAAAGAAAGAAAGCAACATATTGAGTG 658
QY 725 GCTTACAGCGGAGTTCCTTGGAAACAGCCTTCCAGGTTGACGACACAGATAGTCAAA 784
DB 659 GCTTCCGCTTGAATTTCTTGAAGAAAGCGGTTCC---GGCGTGAACATGCGAGATAGTGAA 715
QY 785 ACCTAAGAGCGCAGACCGGAGAGTGAAGAAAGAGAGGAGCCATTGTGACAGTGAAGGAGGCC 844
DB 716 ACCTAAGAGTGAAGAACGAGAGGAGGAGTAGTGGAGCCATTGTGACAGTGAAGAGGAGTC 775
QY 845 TCAGAAATCTTGAAGCCAG---ATAGAAAGAGAGCTGCCGACGAAAGAGAGAAATACGATG 901
DB 776 TAAGAGTCAACAGCTCCAGCCATGAGGAGGACGACAGCAAGAAAGATGATGATGATGATGAGG 835
QY 902 AAGATCAATATGAAATACGATGAAGAGGATGAAGAGGCTGGCAGGGGAAAGCAGAGGAGCGG 961
DB 836 AAGAGCAGCCACAGTGGTGGAGACAGACAAAGGTTGCCAACGCCCAAGCAAAAGGAGCA 895
QY 962 GGAATGGTATTGAAGAGACGATCTGCACCGCAAGTCTAAAGAGAGTCTAAAGAAACATTTGGTAGAAACA 1021
DB 896 GAATGGCATTTGATGAGACCATTTGCAATAGAGCTTCCCAAAACATTTGGTCAGAAAT 955
QY 1022 GATCCCTGACATCTACAAACCCCTCAAGCTGGTTCACTCAAAACCTGCCAACGATCTCAACC 1081
DB 956 CATCACTGACATCTACAAACCCCTCAAGCTGGTAGCATCACAAACGCCACCGCCTTGACT 1015
QY 1082 TTCATAATCTAGTGGCTTGGACCTAGTCTGTAATATGAAATCTCTACAGGAATGTCAT 1141
DB 1016 TCCAGCCCTCTGGCTTCTCAAACTCAGTCCCGCATGATGATCACTCCGCAAGAAATGCTA 1075
QY 1142 TGTTCCTGCTCACTACAAACACCAACGACACAGCATCATATATCGATTGAGGGGACGG 1201
DB 1076 TGTTCGTCACACTACACCTGAAACGCAAGCATATATATACGATTTGAATGGGCGG 1135
QY 1202 CTCAGCTGCAAGTCTGGAGACGACAAACGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1261
DB 1136 CATTTGTAACAGTGGTGAATTCGAATGGTGAGAGAGTGTGATGGAGAGCTGCAAGAG 1195
QY 1262 GTCAGTGTGTTGGTGGCCACAGAACTTCGCGTTCGCTGGAAAGTCCGAGAGCGAAGCT 1321
DB 1196 GAGGGTGTGATGCTGTTCCACAAACTTTGCGGTGGCTGCTCAAAATCCGAGAGCGATAACT 1355
QY 1322 TCGAATACCTGTCATTCAAGACAGACTCAAGGCCACAGCATAGCAACCTTCGCGGTGAA 1381
DB 1256 TTGATGATGTCATTCAAGACCAATGATAGACCTTCGATCGAAACCTTTCAGGGGCAA 1315
QY 1382 ACTCCGTCTATAGATAACCTGCGGAGGAGGTGGTTGCAAAATTCATATGGCTCCAAAGGG 1441
DB 1316 ACTCATTTGTAACCGCATTTGCCAGAGGAAGTATTTCAGCACACTTTTAACCTAAAGAGCC 1375
QY 1442 AGCAGCAAGGAGCTTAAAGAACAAACCCCTTCAAGTTCTTCTGTTCCACCGTCTCAGC 1501
DB 1376 AGCAGCCAGGAGGTGAAGAAACAAACCCCTTTCAGCTTCTTCTGTTCCACCTCAGGAGT 1435
QY 1502 AGTCTCCAGGCGCTGTCGCTTA 1523
DB 1436 CTCAGAGGAGAGCTGTGGCTTA 1457

RESULT 11
US-09-758-652-12
; Sequence 12, Application US/09758652
; Patent No. 6703544
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996

ATTORNEY/AGENT INFORMATION:

NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-758-652-12

Query Match 33.1%; Score 504; DB 3; Length 1458;
Best Local Similarity 62.0%; Pred. No. 2-2e-135;
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;

5 AGCAACCGGAGGAGAACGGGTCCAGTTCAGCGCTCAATGCGCAGAGACCTGACAATC 64
62 AGCAGGCACAGCAAAATGAGTGCAGATCCAAAAGCTGAATGCCCTCAAAACGGATAACC 121
65 GCATTGAATCAGAGGGGGTTACATTGAGACTTGGAAACCCACACACAGGAGTTCGAAT 124
122 GTATAGATCGGAAGGTGGGTTCATTGAGACATGGAAACCCCTAACAAAGCCCAATCCAGT 181
125 GCGCCGGCTGCGCCCTCTCTCGCTTAGTCTCGCGCGCAACGCCCTTCGTAGGCCCTTCT 184
182 GTGCCGGTGTGCGCTCTCTCGCTGCACCCCTTAACCGCAATGCCCTTCGTAGACCTTCT 241
185 ACTCCAAATGTCGCCAGGAGATCTTCATTCAGCAAGAGGGGATACCTTGGGTTCATAT 244
242 ACACCAACGGTCCCGAGGAATCTACATACAAAGGTAATGTATTTTGGCATGATAT 301
245 TCCCTGGTCTCTAGACACTATGAGAGCCTCACACAAAGTTCGTTCGATCTCAGTCCC 304
302 TCCCGGGTGTCTAGCACTTATCAAGAGCCGCA----- 335
305 AAAGACCACCAAGACGCTCTCCAAGGAGAGAACCAAGCCCAACAGCAACGAGATAGTCACC 364
336 -----AGAAATCTCAGCAACGAGGACGAGCCAGAGCCCAAGACCGTCACC 382
365 AGAAGGTGCAACGGTTTCGATGAGGGTGAATCTATTGAGTTCCTCCACGGGTGGCTTCT 424
383 AAAAGGTACATCGCTTCAGAGAGGGTGAATTTGATCGCAGTGCCTACTGTGTGTCATGGT 442
425 GCGCTTACACACGACCAAGACACTGATGTTCTGCTGTTCTTACTGACACCAACAACA 484
443 GGATGTACAAACAATGAAGACACTCCTGTTGTCGGTTCTTATTTGACACCAACAGCT 502
485 ACACCAACCAAGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACACCGGACAG 544

503 TGGAGAACCCAGCTCGACCAGATGCCTAGGAGATTCTATCTTGTGGGAACCAAGACCAAG 562
545 AGTTCTTAAGGTACCAGACGAAACAAAGACGACAAAGACGAAAGACCTTACCATATAGCC 604
563 AGTTTCTAAATATCAGCAGCAG----- 585
605 CATACAGCCCCCAAGTTCAGCTAGACAAAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
586 -----CAGCAAGGAGGTT 598
665 ACAGCCGACAGAAACGAGCAGGACAAAGAAAGAAACGAAAGTGGAAACATCTTCAGCG 724
599 CCAAAAGCCAGAAAGGAAAGCAACAAAGAAAGAAACGAAAGCAACATATTGAGTG 658
725 GCTTCAGCGCGAGTTCCTGGAAACAGCCTTCCAGGTTCCACGACACAGACAGATAGTCAAA 784
659 GCTTCGCCCCCTGAATTTCTTGAAGAAAGCGCTTC---GGCGTGAACATGCGAGATAGTGAGAA 715
785 ACCTAAGAGCGCAGACCGAGAGTGAAAGAGAGGAGGCCATTGTGACAGTGAAGGGGAGGCC 844
716 ACCTACAGGTGAGAACGAGAGGAGGATAGTGGAGCCATTGTGACAGTGAAGGAGGTC 775
845 TCAGAAATCTTGAGCCCCAG---ATAGAAAGAGACGTGCCCGACGAAAGAGGAAATACGATG 901
776 TAAGAGTCAAGCTCCAGCCATGAGGAAGCCACAGCAAGAAAGATGATGATGAGG 835
902 AAGATGAATATGAATACGATGAAGAGGATAGAGGCGTGGCAGGGGAAACGAGGACGG 961
836 AAGAGCAGCCACAGTGCCTGGAGACAGACAAAGGTTGCCAACGCCCAAGCAAAAGAGCA 895
962 GGAATGGTATTGAAGAGACGATCTGCACCGCAGTCTCAAAAGTCTAAAAAGAAACATTTGGTAGAAAA 1021
896 GAAATGGCATTTGATGAGACCATTTGCACAAATGAGACTTCGCCAAAACATTTGGTCAGAA 955
1022 GATCCCTTCACATCTCAACCCCTCAAGCTGGTTTCACTCAAAAGTGCACACGATCTCAACC 1081
956 CATCACTGACATCTACAACCCCTCAAGCTGGTAGCATCAACACCGCCACGAGCTTGACT 1015
1082 TTCTAATCTTAGTGGCTTGGACCTAGTCTGAATATGAAATCTCTACAGGAATGCAT 1141
1016 TCCAGCCCTCTGGCTTCTCAAACTCAGTGGCCAGTATGATCCTCCGCAAGAAATGCTA 1075
1142 TGTTCCTCGCTCACTACAAACACCAACGACACAGCATCATATATCGATTGAGGGGACGG 1201
1076 TGTTCGTGCCACACTACACCTGACCGCAACAGCATATATACGCAATTTGAATGGCGGG 1135
1202 CTCACGTGCAAGTCTGTGGAACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1261
1136 CATTCGTACAAGTGGTGAATTCGAATGGTGAAGAGTGTTCGATGAGAGCTGCAAGAGG 1195
1262 GTCACGTGCTTGTGGTGCCACAGAACTTCGCGCTCGCTGAAAGTCCCAGAGCGAGAACT 1321
1196 GAGGGGTGCTGATTCGTTCCAAACCTTTGCGGTGGCTGCAAAATCCCAGAGGCGTAAT 1255
1322 TCGAATACGTGGCAATTCAGACAGACTCAAGGCCACGATAGCCAACTTCGCGGTGAAA 1381
1256 TTGAGTATGTGTCAATCAAGACCAATGATAGACCCCTCGATCGGAAACCTTGCAGGGGCA 1315
1382 ACTCCGTATAGATAACCTTCGCGGAGGAGTGGTTCGAATTCATATGCGCTTCAAGGG 1441
1316 ACTCATTTGTAACGCAATTCGCCAGAGGAAGTGAATTCAGCACACTTTTAACTTAAAGAGCC 1375
1442 AGCAGCAAGGAGCTTAAAGAAACAAACCCCTTCAAGTTCTTCGTTCCACCGCTCTCAGC 1501
1376 AGCAGCCACAGGAGGTTGAAGAAACAAACCCCTTCAAGTTCTTCGTTCCACCGCTCTCAGC 1435
1502 AGTCTCCGAGGGCTGTGGCTTA 1523
1436 CTCAGAGAGAGCTGTGGCTTA 1457

RESULT 12

US-10-684-651-12

Sequence 12, Application US/10684651
Patent No. 6828491
GENERAL INFORMATION:
APPLICANT: ANTHONY JOHN KINNEY
APPLICANT: GARY MICHAEL FADER
TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
CLASSES OF SOYBEAN SEED
PROTEIN GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/684,651
FILING DATE: 14-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,652
FILING DATE: 11-Jan-2001
APPLICATION NUMBER: 60/019,940
FILING DATE: JUNE 14,1996
ATTORNEY/AGENT INFORMATION:
NAME: LYNNE M. CHRISTENBURY
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1071-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-684-651-12

Query Match 33.1%; Score 504; DB 3; Length 1458;
Best Local Similarity 62.0%; Pred. No. 2.2e-135;
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;
QY 5 AGCAACCGAGGAGAACGGGTGCGAGTCCAGCGCCTCAATGCCGAGACCTGACAAATC 64
DB 62 AGCAGGCACAGCAAAATGATGGCCAGATCCAAAAGCTGAATGCCCTCAAAACCGGATAACC 121
QY 65 GCATTGAATCAGAGGGCGGTACATTGAGACTTGGAAACCCCAACACACAGGAGCTTCAAT 124
DB 122 GTATAGATCGGAAGTGGGTTCATTGAGCATGGAAACCCCTAACACAGCCATTCAGT 181
QY 125 GCGCCGGCGTGCCTCTCTCGTTAGTCTCCGCGCCCAACGCCCTTCGTAGGCGCTTCT 184
DB 182 GTCCGGGTGTGCCCTCTCTCGTGCACCCCTTAACCGCAATGCCCTTCGTAGACCTTCT 241
QY 185 ACTCCAATGTCCTCCAGGAGATCTTCATCCAGCAAGAGGGGATACTTTGGTTCATAT 244
DB 242 ACACCAACCGTCCCGAGAAATCTACATACAAAGGTAATGGTATTTTGGCATGATAT 301
QY 245 TCCCTGTTCTCTAGACACTGAAGAGGCTCACACACAAGGTCTCGATCTCAGTCCC 304
DB 302 TCCCGGGTGTCTAGCACTTATCAAGAGCCGA----- 335
QY 305 AAAGACCACCAAGACGCTCTCCAGGAGAGAACCAAGCCCAACAGCATAGTCACC 364

DB 336 -----AGAATCTCAGCAACGAGGACGAAGCCAGAGGCCCCCAAGACCGTCACC 382
QY 365 AGAAGGTGCACCGTTTCGATGAGGGTGATCTCATTCGAGTTCCACCGGTGTTGCTTCT 424
DB 383 AAAGGTACATCGCTTCAGAGAGGGTGATTTGATCGAGTGCCTACTCTGGTGTTCATGGT 442
QY 425 GGCTCTACAACGACCAACGACACTGATGTTGTTGCTGTTCTTCTTACTGACCAACAACA 484
DB 443 GGATGTACAACAATGAAGACACTCTCTGTTGTCGCGTTCTCTAATTAACCAACAGCT 502
QY 485 ACAGAACACGACTTGATCATGTTCCCGAGGAGATTCAATTTGGCTGGGAACACCGAGCAAG 544
DB 503 TCGAGAACCGAGCTCGACCAAGTGCCTAGGAGATTCTATCTTGTCTGGGAACCAAGCAAG 562
QY 545 AGTTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGACGAAGAGCTTACCATATAGCC 604
DB 563 AGTTTCTAAATATCAGCAGCAG----- 585
QY 605 CATACAGCCCGCAAAAGTTCAGCCTTAGACAAGAAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
DB 586 -----CAGCAAGGAGGTT 598
QY 665 ACAGCCGACAGAAACGAGCAGGACAGAAAGAAAGAAACGAAGGTGAAACATCTTCAGCG 724
DB 599 CCAAAAGCCAGAAAGGAAAGCAACAGAAAGAAAGAAACGAAGAAACATATTGAGTG 658
QY 725 GCTTCACGCGGAGTTCTTGGAAACAGCCTTCCAGGTTGACGACAGACAGATAGTCAAA 784
DB 659 GCTTCGCCCTGAAATCTTGAAGAAGCGTTC---GGCGTGAACATGACAGATAGTGAGAA 715
QY 785 ACCTAAGAGGCGAGACCGAGAGGTGAAGAAGAGGGAGCCATTGTGACAGTGAAGGGAGGCC 844
DB 716 ACCTAAGGTGAGAACGAAGAGGAGGATAGTGGAGCCATTGTGACAGTGAAGAGGAGTGC 775
QY 845 TCAGAAATCTTGAGCCAG---ATAGAAAGAGACGTGCCGACGAGAGAGGAAATAGCATG 901
DB 776 TAAGAGTCAAGTCCAGCCATGAGGAAGCCACAGCAAGAAGAAGATGATGATGATGAGG 835
QY 902 AAGATGAATATGAATACGATGAAGAGGTAGAGGCGTGGCAGGGGAAGCAGAGGAGGG 961
DB 836 AAGAGCAGCCAGTGCCTGGAGACAGACAAGGTTGCCAACGCCAAAGCAAGAAAGAGCA 895
QY 962 GGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGCTTAAAGAAACAATTGGTGAAGACA 1021
DB 896 GAAATGGCATTCAGAGACCATTTGCACAATGAGACTTCGCCCAAAACATTTGGTCAGAA 955
QY 1022 GATCCCTGACATCTCAACCCCTCAAGCTGGTTCACCTCAAAACCTGCCAACGATCTCAACC 1081
DB 956 CATCACTGACATCTCAACCCCTCAAGCTGGTGAACATCAACCCGCCACCGAGCTTGAAT 1015
QY 1082 TTCTAATAGTCTAGGTGGCTTGGACCTTAGTCTGAATATGGAATCTCTACAGGAATGCAT 1141
DB 1016 TCCAGCCCTCTGGCTTCTCAAACTCAGTGCCTCAGTATGGATCCTCCGCAAGATGCTA 1075
QY 1142 TGTGTTGCTCCTACACACCAACGACACAGCATCATATATCATGATTGAGGGGACGG 1201
DB 1076 TGTGTCGCCACACTACACCCCTGAAACGCAACAGCATAATATACGCAATGAAATGGCGGG 1135
QY 1202 CTCACGTGCAAGTGTGGACAGCAACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGG 1261
DB 1136 CATTTGTCAAGTGGTGAATTGCAATGGTGAAGAGTGTGTTGAGAGAGTGCACAGAGG 1195
QY 1262 GTCAGCTGCTTGTGTGTCACAGAACTTCGCGTCCGTAAGTCCAGAGGAGGAGAACT 1321
DB 1196 GAGGGGTGCTGATTCGTTCCCAAAACCTTTGGGTGGCTGCAAAATCCAGAGGAGTAACT 1255
QY 1322 TCGAATACGTGGCATTCAGACAGACTCAAGGCCACAGCATAGCCAACTCGCCGGTGAAA 1381
DB 1256 TTGAGTATGTGATTCAGAGACCAATGATAGACCTCGATCGGAAACCTTGCAGGGGCAA 1315
QY 1382 ACTCCGCTCATAGATAACCTGCGGAGGAGGTGGTTCGCAATTCATATGCGCTTCAAGGG 1441
DB 1316 ACTCATTTGTAAGCGATTTGCCAGAGGAGTGAATTCAGCACACTTTTAAACCTTAAGAGCC 1375

Db 1311 TGAGCTAAGGAGGCAATTTGCTAGTGGTCCGACAGACCCGCGTGGCTGAGCAAGG 1370
QY 1308 CCAGAGCGAGAACTTCCAAATACGTGGCACTTCAAGACAGAC 1347
Db 1371 GGAGAGCAAGGATTGGAATATGATGTTTCAAGACACAC 1410

RESULT 14
US-09-758-652-15
; Sequence 15, Application US/09758652
; Patent No. 6703544
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14,1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-758-652-15

Query Match 13.0%; Score 198; DB 3; Length 1551;
Best Local Similarity 51.4%; Pred. No. 1e-46;
Matches 699; Conservative 0; Mismatches 600; Indels 61; Gaps 8;
QY 14 AGGAGAACCGTGCCAGTTCAGCGCTCAATCGCAGAGACTGACAAATCGCAATGAAT 73
Db 86 AGTTCACAGAGTGCCAACTCAACAACTCAACCGCTTGGAAACCCGACACCGCGTTGAGT 145
QY 74 CAGAGGCGGTACATTGAGACTTGGNAACCCCAACACAGGATTCGAATGCGCGCG 133
Db 146 CCGAAGGTGGTCTTATTTGAACATGAACTCTCAACACCGCTGAGCTGCAATGCGCGGTG 205
QY 134 TCGCCCTCTCTCGCTTAGTCTCCGCGCAACCGCTTCGTAGCCCTTTCTACTCCAATG 193
Db 206 TCACTGTTCCAAACGACCCCTCAACCGCAACGGCTCCCACTTGGCCATCTTACTTACCTT 265
QY 194 CTCCCCAGGAGATCTTCATCCAGCAAGGAGGGGATACCTTGGGTTGATTTCCCTGGTT 253
Db 1311 TGAGCTAAGGAGGACAAATTGCTAGTGGTCCGACAGAACCCCGCGTGGCTGAGCAAGG 1370

Db 266 ATCCCAAAATGATCATTTGCTGTTCAAGGAGGAGCAATTTGATTTTTCATTTTCCGGAT 325
QY 254 GTCTTAGACACTATGAAGAGCCTCACACACAAGGTGCTGATCTCAGTCCCAAGACAC 313
Db 326 GTCCGAGAGCTTTGAGAGCCACA-----ACAA 355
QY 314 CAAGACGTCTTCAAGGAGAGCAAAAGCCAAAGCAAGCAAGATAGTACCAGAGGTGC 373
Db 356 AATCAAGCAGAGAGGCTCAAGGTCAAGCAGCAACTACAAGACAGTACCAGAGATTC 415
QY 374 ACCGTTTCGATGAGGTGATCTCATTTGCAAGTCCCAAGGTGCTTCTTGGCTCTACA 433
Db 416 GTCACTTCAATGAAGGAGAGCGTACTAGTGTCTCTTGGTGTCTTACTGACCTATA 475
QY 434 ACACACGACACTGATGTTGTTGCTTCTTACTGACACCAACAAACAGCAAC 493
Db 476 AACTGGGATGACACGATTTGTCATCTTGGACCTCAACTTCAACATC 535
QY 494 AGCTTGATCAGTTTCCCAGGAGATTCAATTTGGCTGGGAACACGGAGCAAGTCTTAA 553
Db 536 AGCTTGATCAAAACCCAGAGTATTTTACCTTCTGGAAACCCAGATATAGACATCCG 595
QY 554 GGTACAGCAACAAAGCAGACAAAGCAGAGCAAGAGCTTTACCATATAGCCCATACAGCC 613
Db 596 AGACCATGCAACAA--CAGCAGCAGCAGAGAGTCTATGTTGGACGCAAGCAGGCGCAACA 653
QY 614 CGCAAGTCAAGCTAGACAAAGAG-AGCGTGAATTTAGCCCTCGAGGACAGCAGCCG 672
Db 654 CGACAGCAGGAGGAAGAGGTGGCAGTGTCTCAGTGGCTTCAGCAACATTTCTTAGC 713
QY 673 AGAGAACGAGCAGGACAAAGAAAGAAACGAGGTGGAAACAATCTTCAG-----CGCTT 728
Db 714 ACAATCTTTCAACACCAACAGGACACAGCTGAGAAACTTCGGTCTCCAGATCAGCAAG 773
QY 729 CAGCCGAGTTCCTGGAACAGCCTTCCAGGTTGACGACAGACAGATAGTGGAAACCT 788
Db 774 GAAGCAGATCGTGACAGTGGAGGCGCTCAGCGTTATCAGCCCAAGTGGCAAGACA 833
QY 789 AAGAGCGAGACCGAGAGTGAAGAGGAGGAGCATTGTCAGAGTGGAGGAGGCGCTCAG 848
Db 834 AGAGACGAGAGAGAGACGAAAGACGAAAGATATGGAACGACGCCCTTTATCTCTCAGC 893
QY 849 AATCTTTGAGCCAGATAGAAAGAGAGCGTGC---GACGAAGAGAGAGAAATACGATGAAGA 905
Db 894 ACAGCAACCCATCGAAACCATGAGATCAGCAGGACGAGGACGAGAGAGAGAAAGATCAACC 953
QY 906 TGAATATGATACGATGAAGAGATAGAAG-----CGTGGCAGGGG 947
Db 954 TCGTCTGATCACCTCCACAGCGACCAAGCAGGCGCCGAAACAAAGAACACACGCTGGAAG 1013
QY 948 AAGCAGGCGAGGGGAATGGTATTGAAGAGACGATCTCAGCCGCAAGTCTTAAAGAA 1007
Db 1014 AGGATGTACAGCTAGAAATGGGGTTGAGGAAATATTTGACCATGAAGCTTCAAGAGAA 1073
QY 1008 CATTTGTGAGAAACAGATCCCTTGACATCTACAACCTCAAGCTGGTTCATCAAAACTGC 1067
Db 1074 CATTTGCTGCCCTTCAAGCTGCTGACTTCTACAACCCCAAGCTGGTGGCATTAGCACCT 1133
QY 1068 CAAAGATCTCAACCTTCTAATATCTTAGTGGCTTGGACCTAGTGTGAAATATATGAAATCT 1127
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QY 1128 CTACAGGATGATGTTTGTGCTCACTACAACACCAAGCAGCAGCATCATATATCG 1187
Db 1194 CTACAGGATGAAATTTACTCTCCAGATTGGAATTTGAACGCAAGCAGTGTGACG-ATGA 1252
QY 1188 ATTGAGGAGACGGGCTCACGTCAAAGTCTGTGACAGCAACCGCAACAGAGTGTACAGCA 1247
Db 1253 CTCGAGGGAAG--AAGAGTTAGAGTGTGTAACCTGCCAAGGGAATGCAAGTGTTCGACGG 1310
QY 1248 GGAGCTTCAAGAGGTCAGTCTTGTGTCAGCAAGAACTTCCGCGTCCGCTGGAAAGTC 1307
Db 1311 TGAGCTAAGGAGGACAAATTGCTAGTGGTCCGACAGAACCCCGCGTGGCTGAGCAAGG 1370

QY 1308 CCAGACGAGAACTTCGAATACGTGCAATTCAGACAGAC 1347
Db 1371 GGGAGAACAAAGGATGGAATATAGTAGTTCAGACACAC 1410

RESULT 15
US-10-684-651-15
; Sequence 15, Application US/10684651
; Patent No. 6828491
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; APPLICANT: GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/684,651
; FILING DATE: 14-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14,1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Query Match 13.0%; Score 198; DB 3; Length 1551;
Best Local Similarity 51.4%; Pred. No. 1e-46;
Matches 699; Conservative 0; Mismatches 600; Indels 61; Gaps 8;

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Job time : 251.534 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2006, 18:12:55 ; Search time 2083.24 Seconds
(without alignments)
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main:*

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- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1524	100.0	1524	6	US-10-728-806-5
3	1524	100.0	1524	9	US-10-100-303A-89
4	1524	100.0	1524	9	US-10-728-323-3
5	1524	100.0	1524	9	US-10-728-051-3
6	1524	100.0	1524	10	US-10-899-551-5
7	1391.2	91.3	1853	10	US-10-958-324-4
8	517.4	34.0	1446	8	US-09-758-652-13
9	517.4	34.0	1446	8	US-10-684-651-13
10	517.4	34.0	1446	8	US-10-757-074-13
11	517.4	34.0	1446	8	US-10-757-155-13
12	517.4	34.0	1446	8	US-10-757-667-13
13	517.4	34.0	1446	10	US-10-508-263-27
14	517.4	34.0	1673	8	US-10-425-114-7280
15	517.4	34.0	1689	8	US-10-425-114-8531
16	517.4	34.0	1694	8	US-10-425-114-8592
17	517.4	34.0	1697	8	US-10-425-114-7583

18	517.4	34.0	1766	8	US-10-424-599-28860	Sequence 28860, A
19	515.8	33.8	1671	8	US-10-425-114-7594	Sequence 7594, Ap
20	513	33.7	1431	10	US-10-409-993-2	Sequence 2, Appli
21	513	33.7	1434	10	US-10-409-993-16	Sequence 16, Appl
22	513	33.7	1458	10	US-10-409-993-10	Sequence 10, Appl
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24	513	33.7	1488	8	US-10-684-651-11	Sequence 11, Appl
25	513	33.7	1488	8	US-10-757-074-11	Sequence 11, Appl
26	513	33.7	1488	8	US-10-757-155-11	Sequence 11, Appl
27	513	33.7	1488	8	US-10-757-667-11	Sequence 11, Appl
28	513	33.7	1488	10	US-10-508-263-19	Sequence 19, Appl
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30	513	33.7	1716	8	US-10-425-114-8556	Sequence 8556, Ap
31	513	33.7	1718	8	US-10-425-114-7642	Sequence 7642, Ap
32	513	33.7	1721	8	US-10-425-114-7670	Sequence 7670, Ap
33	513	33.7	1724	8	US-10-425-114-7613	Sequence 7613, Ap
34	513	33.7	1724	8	US-10-425-114-8587	Sequence 8587, Ap
35	513	33.7	1727	8	US-10-425-114-7603	Sequence 7603, Ap
36	513	33.7	1727	8	US-10-425-114-7624	Sequence 7624, Ap
37	513	33.7	1729	8	US-10-425-114-8164	Sequence 8164, Ap
38	513	33.7	1730	8	US-10-425-114-8133	Sequence 8133, Ap
39	513	33.7	1834	8	US-10-424-599-28863	Sequence 28863, A
40	511.4	33.6	1458	10	US-10-409-993-14	Sequence 14, Appl
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42	505	33.1	1746	3	US-09-805-694B-15	Sequence 15, Appl
43	505	33.1	1746	9	US-10-922-732-15	Sequence 15, Appl
44	504	33.1	1458	3	US-09-758-652-12	Sequence 12, Appl
45	504	33.1	1458	8	US-10-684-651-12	Sequence 12, Appl

ALIGNMENTS

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US-09-731-375A-3
; Sequence 3, Application US/09731375A
; Publication No. US20030035810A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0100
; CURRENT APPLICATION NUMBER: US/09/731,375A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Atacis hypogaea
US-09-731-375A-3

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				Indels	0;
				Gaps	0;
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US-10-228-806-5
; Sequence 5, Application US/10228806
; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannon, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0043
; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1524
; TYPE: DNA
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US-10-728-323-3
; Sequence 3, Application US/10728323
; Publication No. US2004020894A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0232
; CURRENT APPLICATION NUMBER: US/10/728,323
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,035
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: DNA
; ORGANISM: Arachis hypogaea
; US-10-728-323-3

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Db 61 AATCGCATTTGAATCAGAGGGCGGTTACATTGAGACTTTGGAAACCCCAACACAGGAGTTTC 120
QY 121 GAATGCGCGGGCGTCCGCCCTCTCTCGCTTAGTCTCCCGCGCAACGCCCTTCGTAGGCCCT 180
Db 121 GAATGCGCGGGCGTCCGCCCTCTCTCGCTTAGTCTCCCGCGCAACGCCCTTCGTAGGCCCT 180
QY 181 TTCTACTCCAATGCTCTCCAGAGAGATCTTCATCCAGCAAGAGGGGATACCTTTGGGTTG 240
Db 181 TTCTACTCCAATGCTCTCCAGAGAGATCTTCATCCAGCAAGAGGGGATACCTTTGGGTTG 240
QY 241 ATATTCCCTGGTGTCTTAGACACTATGAAGAGCCTCACACAAAGTCTCGTATCTCAG 300
Db 241 ATATTCCCTGGTGTCTTAGACACTATGAAGAGCCTCACACAAAGTCTCGTATCTCAG 300
QY 301 TCCCAAGACACCAAGAGAGTCTTCCAAAGGAGAGAGCAAAAGGCCAAACAGCAACAGAGATAGT 360
Db 301 TCCCAAGACACCAAGAGAGTCTTCCAAAGGAGAGAGCAAAAGGCCAAACAGCAACAGAGATAGT 360
QY 361 CACCAAGAGGTGCACCGTTTCGATGAGGGTGATCTCAITTCAGTTCCTCCACCGTGTGCT 420
Db 361 CACCAAGAGGTGCACCGTTTCGATGAGGGTGATCTCAITTCAGTTCCTCCACCGTGTGCT 420
QY 421 TTCTGCTCTCAACACGACCAACGACACTGATGTTGTTGCTGTTCTCTTACTGACACCAAC 480
Db 421 TTCTGCTCTCAACACGACCAACGACACTGATGTTGTTGCTGTTCTCTTACTGACACCAAC 480
QY 481 AACCAACGACCAACCCAGCTTGATCAGTTTCCCAGGAGATTCAATTTGGCTGGGAAACAGGAG 540
Db 481 AACCAACGACCAACCCAGCTTGATCAGTTTCCCAGGAGATTCAATTTGGCTGGGAAACAGGAG 540
QY 541 CAAAGATGTTTAAAGTTACAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT 600
Db 541 CAAAGATGTTTAAAGTTACAGCAACAAAGCAGACAAAGCAGACGAAAGAGCTTACCATAT 600
QY 601 AGCCCATACAGCCCGCAAAAGTACGCTTAGACAAGAGAGCGTCAATTTAGCCCTTCGAGGA 660
Db 601 AGCCCATACAGCCCGCAAAAGTACGCTTAGACAAGAGAGCGTCAATTTAGCCCTTCGAGGA 660
QY 661 CAGCAGACCGCGCAGAGAAACGAGCAGGACCAAGAAAGAAAGAAACGAAAGTGGAAACATCTTC 720
Db 661 CAGCAGACCGCGCAGAGAAACGAGCAGGACCAAGAAAGAAAGAAACGAAAGTGGAAACATCTTC 720
QY 721 AGCGGCTTCAACGCGGAGTTCTTGGAAACAAAGCCCTTCAGGTTGACGACAGACAGATAGTG 780
Db 721 AGCGGCTTCAACGCGGAGTTCTTGGAAACAAAGCCCTTCAGGTTGACGACAGACAGATAGTG 780
QY 781 CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA 840
Db 781 CAAAACCTTAAGAGCGGAGACCGGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA 840
QY 841 GGCCTCAGAAATCTTGAGCCCGCAGATAGAAAGAGAGCGTGCCTCCGACGAAGAAGAGGAATACGAT 900
Db 841 GGCCTCAGAAATCTTGAGCCCGCAGATAGAAAGAGAGCGTGCCTCCGACGAAGAAGAGGAATACGAT 900
QY 901 GAAGATGAATATGAATACGATGAAGAGGATAGNAGGCGTGGCAGGGAAGCAGAGCGAG 960
Db 901 GAAGATGAATATGAATACGATGAAGAGGATAGNAGGCGTGGCAGGGAAGCAGAGCGAG 960
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QY 961 GGAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTCTAAAAAGAACATTGGTAGAAG 1020
DB 961 GGAATGGTATTGAAGAGAGCGATCTGCACCGCAAGTCTAAAAAGAACATTGGTAGAAG 1020
QY 1021 AGATCCCTGACATCTACAAACCTCAAGCTGGTTCACCTAAAAGTGCACGATCTCAAC 1080
DB 1021 AGATCCCTGACATCTACAAACCTCAAGCTGGTTCACCTAAAAGTGCACGATCTCAAC 1080
QY 1081 CTTCTAATCTAGGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCA 1140
DB 1081 CTTCTAATCTAGGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCA 1140
QY 1141 TTGTTTGTCTCCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGACGG 1200
DB 1141 TTGTTTGTCTCCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGACGG 1200
QY 1201 GCTCAGTGAAGTCTGAGGAGAGCAAGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260
DB 1201 GCTCAGTGAAGTCTGAGGAGAGCAAGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG 1260
QY 1261 GGTCAAGTGTGTTGGTGGCAGAGACTTTCGCGTCTGCTGGAAGTCCAGAGCGAGAAC 1320
DB 1261 GGTCAAGTGTGTTGGTGGCAGAGACTTTCGCGTCTGCTGGAAGTCCAGAGCGAGAAC 1320
QY 1321 TTGGAATACGTGGCATTTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAA 1380
DB 1321 TTGGAATACGTGGCATTTCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAA 1380
QY 1381 AACTCCGTATAGATTAACCTGCGGAGGAGTGGTTCGAAATTCATATGGCTTCCAAAGG 1440
DB 1381 AACTCCGTATAGATTAACCTGCGGAGGAGTGGTTCGAAATTCATATGGCTTCCAAAGG 1440
QY 1441 GAGCAGGAGGAGCTTAAGAACACACACCCCTTCAAGTCTCTGTTCCACCGTCTCAG 1500
DB 1441 GAGCAGGAGGAGCTTAAGAACACACACCCCTTCAAGTCTCTGTTCCACCGTCTCAG 1500
QY 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524
DB 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524

RESULT 5

US-10-728-051-3
; Sequence 3, Application US/10728051
; Publication No. US20040234548A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Bottomly H., Kim
; APPLICANT: Sosin B., Howard
; APPLICANT: Burks A., Wesley
; APPLICANT: Sampson A., Hugh
; TITLE OF INVENTION: Microbial Delivery System
; FILE REFERENCE: 2002834-0222
; CURRENT FILING DATE: 2003-12-04
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/731,375
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-728-051-3

Query Match 100.0%; Score 1524; DB 9; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCAGCAACCGGAGGAGAACGGTCCAGTTCAGCGGCTCAATGCGCAGAGACCTGAC 60

DB 1 CGGCAGCAACCGGAGGAGAACGGTCCAGTTCAGCGGCTCAATGCGCAGAGACCTGAC 60
QY 61 AATCGCATTTGAATCAGAGGCGGTTACATTGAGACTTGGNACCCCAACACAGAGAGTTC 120
DB 61 AATCGCATTTGAATCAGAGGCGGTTACATTGAGACTTGGNACCCCAACACAGAGAGTTC 120
QY 121 GAATGCGCGGCGCTCCGCTCTCTCGCTTAGTCTCTCGCGCGCAACGCGCTTCGTAGGCT 180
DB 121 GAATGCGCGGCGCTCCGCTCTCTCGCTTAGTCTCTCGCGCGCAACGCGCTTCGTAGGCT 180
QY 181 TTCTACTCCAATGCTCCCGAGGAGATCTTTCATCCAGCAAGGAAGGGGATATTTGGGTTG 240
DB 181 TTCTACTCCAATGCTCCCGAGGAGATCTTTCATCCAGCAAGGAAGGGGATATTTGGGTTG 240
QY 241 ATATTCCCTGGTGTCTAGACACTATGAAGAGCTTCACACAAAGGTCTGATCTCAG 300
DB 241 ATATTCCCTGGTGTCTAGACACTATGAAGAGCTTCACACAAAGGTCTGATCTCAG 300
QY 301 TCCCAAGACACCAAGAGAGCTCTCCAAAGGAGAGACCAAGGCAACAGCAACGAGATAGT 360
DB 301 TCCCAAGACACCAAGAGAGCTCTCCAAAGGAGAGACCAAGGCAACAGCAACGAGATAGT 360
QY 361 CACCAGAGGTGCACCGTTCGATGAGGTGATCTCATTTGACGTTCCACCGGTGTTGCT 420
DB 361 CACCAGAGGTGCACCGTTCGATGAGGTGATCTCATTTGACGTTCCACCGGTGTTGCT 420
QY 421 TTCTGCTCTACACGACCAACGACACTGATTTGTTGCTGTTTCTCTTACTGACCAAC 480
DB 421 TTCTGCTCTACACGACCAACGACACTGATTTGTTGCTGTTTCTCTTACTGACCAAC 480
QY 481 AACACGCAACACGAGCTTGCATCAGTTCCCGAGGAGATTCATTTGGTGGGAAACAGGAG 540
DB 481 AACACGCAACACGAGCTTGCATCAGTTCCCGAGGAGATTCATTTGGTGGGAAACAGGAG 540
QY 541 CAAGAGTCTTTAAGGTACCAGCAACAAAGCAGACGAGAGAGAGTTCACATAT 600
DB 541 CAAGAGTCTTTAAGGTACCAGCAACAAAGCAGACGAGAGAGAGTTCACATAT 600
QY 601 AGCCCATACAGCCCGCAAGTTCAGCTAGACAGAGAGAGAGTTCATTTAGCCCTCAGGA 660
DB 601 AGCCCATACAGCCCGCAAGTTCAGCTAGACAGAGAGAGAGTTCATTTAGCCCTCAGGA 660
QY 661 CAGCAGCGCGCAGAGAACGAGCAGGACCAAGAGAGAGAGAGAGTTCGAAATTCCTTC 720
DB 661 CAGCAGCGCGCAGAGAACGAGCAGGACCAAGAGAGAGAGAGAGTTCGAAATTCCTTC 720
QY 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAGCCTTCAGGTTGACACAGACAGATAGTG 780
DB 721 AGCGGCTTCACGCGGAGTTCCTGGAAACAAGCCTTCAGGTTGACACAGACAGATAGTG 780
QY 781 CAAAACCTTAAGAGGCGAGACCGAGAGTGAAGAGAGAGAGAGTTCGAGAGAGAGAGAG 840
DB 781 CAAAACCTTAAGAGGCGAGACCGAGAGTGAAGAGAGAGAGAGTTCGAGAGAGAGAGAG 840
QY 841 GGCCTCAGAAATCTTAGAGCCAGATAGAAAGAGAGAGTTCGCGACGAAGAGAGAGTTCAT 900
DB 841 GGCCTCAGAAATCTTAGAGCCAGATAGAAAGAGAGAGTTCGCGACGAAGAGAGAGTTCAT 900
QY 901 GAAGATGAATATGAATACGATGAAGAGATAGAGGCGTGGCAGGAGAGAGAGAGAGAGG 960
DB 901 GAAGATGAATATGAATACGATGAAGAGATAGAGGCGTGGCAGGAGAGAGAGAGAGAGG 960
QY 961 GGGATGTTTGAAGAGAGAGATCTGCACCGCAAGTCTTAAAGAGAGAGATTCGTAGAAC 1020
DB 961 GGGATGTTTGAAGAGAGAGATCTGCACCGCAAGTCTTAAAGAGAGAGATTCGTAGAAC 1020
QY 1021 AGATCCCTGACATCTACAAACCTCAAGCTGGTTCATCAAACTCCCAACGATCTCAAC 1080
DB 1021 AGATCCCTGACATCTACAAACCTCAAGCTGGTTCATCAAACTCCCAACGATCTCAAC 1080
QY 1081 CTTCTAATCTAGGTGGCTTGGACCTAGTCTGAATATGGAATTCATAGGAAATCTTACAGGAATGCA 1140

Db	1081	CTTCTAATACTTAGGTGGCTTGGACCTAGTGTGCTGAATATGGAATCTCTACAGGAATGCA	1140
QY	1141	TTGTTTGTGGCTCACTAACAACCAACGACACAGCATCATATATCGATTGAGGGACGG	1200
Db	1141	TTGTTTGTGGCTCACTAACAACCAACGACACAGCATCATATATCGATTGAGGGACGG	1200
QY	1201	GCTCAGTGCAGTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
Db	1201	GCTCAGTGCAGTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
QY	1261	GGTCAAGTCTTTGTGTGGCCACAGAACTTCGCGCTCGCTGGAAAGTCCCGAGCGAGAAC	1320
Db	1261	GGTCAAGTCTTTGTGTGGCCACAGAACTTCGCGCTCGCTGGAAAGTCCCGAGCGAGAAC	1320
QY	1321	TTGGAATAGTGGCATTCAAGACAGACTCAAGGCCACAGATAGCCTCGCGGTGAA	1380
Db	1321	TTGGAATAGTGGCATTCAAGACAGACTCAAGGCCACAGATAGCCTCGCGGTGAA	1380
QY	1381	AATCCGCTCATAGATAACCTGCCGAGGAGGTGGTTGCAAAATTCATATGGCCTCCAAAGG	1440
Db	1381	AATCCGCTCATAGATAACCTGCCGAGGAGGTGGTTGCAAAATTCATATGGCCTCCAAAGG	1440
QY	1441	GAGCAGCAAGGAGCAGCTTAAGAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTCAG	1500
Db	1441	GAGCAGCAAGGAGCAGCTTAAGAACAAACCCCTTCAAGTTCCTGTTCCACCGTCTCAG	1500
QY	1501	CAGTCTCCGAGGCTGTGGCTTAA	1524
Db	1501	CAGTCTCCGAGGCTGTGGCTTAA	1524

RESULT 6
US-10-899-551-5
; Sequence 5, Application US/10899551
; Publication No. US20050063994A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael J.
; APPLICANT: Burks, A. Wesley
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Howard, Sosin B.
; APPLICANT: Bottomly, Kim H.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reaction to Allergy
; FILE REFERENCE: 2002834-0233
; CURRENT APPLICATION NUMBER: US/10/899,551
; CURRENT FILING DATE: 2004-07-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: species Arachis hypogaea
US-10-899-551-5

Query Match	100.0%;	Score 1524;	DB 10;	Length 1524;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1524;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGGACGAAACCGGAGGAGAACCGGTGCGCAGTTCAGGGCCCTCAATGCGGACAGACCTGAC	60	
Db	1	CGGACGAAACCGGAGGAGAACCGGTGCGCAGTTCAGGGCCCTCAATGCGGACAGACCTGAC	60	
QY	61	AATCGCATTGAATCAGAGGCGGTTCATTGAGACTTGGAAACCCCAACACCAAGGAGTTC	120	
Db	61	AATCGCATTGAATCAGAGGCGGTTCATTGAGACTTGGAAACCCCAACACCAAGGAGTTC	120	
QY	121	GAATGCGCGCGGTGCGCCTCTCTCGCTTAGTCTCGCGCGCAACGCGCTTCGTAGCCT	180	
Db	121	GAATGCGCGCGGTGCGCCTCTCTCGCTTAGTCTCGCGCGCAACGCGCTTCGTAGCCT	180	
QY	181	TTCTACTCAGTGTCCCAAGGAGATCTTCATCAGCAAGGAGGGGATACCTTTGGGTG	240	
Db	181	TTCTACTCAGTGTCCCAAGGAGATCTTCATCAGCAAGGAGGGGATACCTTTGGGTG	240	

QY	241	ATATTCCCTGGTTGCTTAGACACTATGAAGAGCCTCACACACAGAGTGTGATCTCAG	300
Db	241	ATATTCCCTGGTTGCTTAGACACTATGAAGAGCCTCACACACAGAGTGTGATCTCAG	300
QY	301	TCCCAAGAACCAACCAAGAGCGTCTTCCAAAGAGAGACCAAGCCCAACAGCAACGAGATAGT	360
Db	301	TCCCAAGAACCAACCAAGAGCGTCTTCCAAAGAGAGACCAAGCCCAACAGCAACGAGATAGT	360
QY	361	CACCAAGAGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAGTTCCCAACCGGTGTTGCT	420
Db	361	CACCAAGAGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAGTTCCCAACCGGTGTTGCT	420
QY	421	TTCTGGCTCTCAACCAAGCACCACGACACTGATGTTGTTGCTGTTTCTCTTACTGACCAAC	480
Db	421	TTCTGGCTCTCAACCAAGCACCACGACACTGATGTTGTTGCTGTTTCTCTTACTGACCAAC	480
QY	481	AACAACGACAAACGAGTTGATCAGTTTCCCAGGAGATTCAATTTGCTGGGAACACGGAG	540
Db	481	AACAACGACAAACGAGTTGATCAGTTTCCCAGGAGATTCAATTTGCTGGGAACACGGAG	540
QY	541	CAAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATAT	600
Db	541	CAAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGACGAAGAAGCTTACCATAT	600
QY	601	AGCCCATACAGCCCGCAAAAGTCAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
Db	601	AGCCCATACAGCCCGCAAAAGTCAGCCTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGA	660
QY	661	CAGCAGCGCGCAGAGAACGAGCAGCAACAAAGAGAGAAACGAAGGTGGAACATCTTC	720
Db	661	CAGCAGCGCGCAGAGAACGAGCAGCAACAAAGAGAGAAACGAAGGTGGAACATCTTC	720
QY	721	AGCGGCTTCAACCGCGGAGTTCTCTGGAAACAAAGCCTTCAGGTTGACACAGACAGATAGTG	780
Db	721	AGCGGCTTCAACCGCGGAGTTCTCTGGAAACAAAGCCTTCAGGTTGACACAGACAGATAGTG	780
QY	781	CAAAACCTAAGAGGCGGAGACCGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA	840
Db	781	CAAAACCTAAGAGGCGGAGACCGAGAGTGAAGAGAGGAGGCCATTGTGACAGTGAGGGGA	840
QY	841	GGCTCAGAAATTTGAGCCGAGATGAAGAGAGCGTGCAGCAAGAAAGAGGAATACGAT	900
Db	841	GGCTCAGAAATTTGAGCCGAGATGAAGAGAGCGTGCAGCAAGAAAGAGGAATACGAT	900
QY	901	GAAGATGAATATGAATACGATGAAGAGGATGAAGAGGCTGGCAGGGGAGCAGGACGG	960
Db	901	GAAGATGAATATGAATACGATGAAGAGGATGAAGAGGCTGGCAGGGGAGCAGGACGG	960
QY	961	GGGAATGGTATTGAAGAGACGATCTGCAACCGCAAGTGTCTGTAAGAAACATTTGGTAGAAAC	1020
Db	961	GGGAATGGTATTGAAGAGACGATCTGCAACCGCAAGTGTCTGTAAGAAACATTTGGTAGAAAC	1020
QY	1021	AGATCCCTGACATCTCAACACCTCAAGCTGGTTCATCTCAAACTGCCAACGATCTCAAC	1080
Db	1021	AGATCCCTGACATCTCAACACCTCAAGCTGGTTCATCTCAAACTGCCAACGATCTCAAC	1080
QY	1081	CTTCTAATCTAGTGGCTTGGACCTAGTGTCTGAATATGGAATCTCTACAGGAATGCA	1140
Db	1081	CTTCTAATCTAGTGGCTTGGACCTAGTGTCTGAATATGGAATCTCTACAGGAATGCA	1140
QY	1141	TTGTTTGTGCTCACTAACAACCAACGACACAGCATATATCGATTGAGGGACGG	1200
Db	1141	TTGTTTGTGCTCACTAACAACCAACGACACAGCATATATCGATTGAGGGACGG	1200
QY	1201	GCTCAGTGCAGTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
Db	1201	GCTCAGTGCAGTGTGGACAGCAACGCGCAACAGAGTGTACGACGAGGAGCTTCAAGAG	1260
QY	1261	GGTCAAGTGTGTTGGTGCACAGAACTTCGCGCTCGCTGGAAAGTCCCAAGCGAGAAC	1320
Db	1261	GGTCAAGTGTGTTGGTGCACAGAACTTCGCGCTCGCTGGAAAGTCCCAAGCGAGAAC	1320
QY	1321	TTGGAATAGTGGCATTTCAAGACAGACTCAAGGCCACAGATAGCCTCGCGGTGAA	1380

Db 1321 TTGGAATACGTGGCAATTCAGACAGACTCAAGGCCAGCATAGCAAACCTCGCGGTGAA 1380
Qy 1381 AACTCCGCTCATAGATAACCTGCGGAGGAGTGTGCAAAATTCATATGCGCTCCRAAGG 1440
Db 1381 AACTCCGCTCATAGATAACCTGCGGAGGAGTGTGCAAAATTCATATGCGCTCCRAAGG 1440
Qy 1441 GAGCAGCAAGGCGAGCTTAAAGAACAAACCCCTTCAAGTTCCTCGTTCCACCGTCTCAG 1500
Db 1441 GAGCAGCAAGGCGAGCTTAAAGAACAAACCCCTTCAAGTTCCTCGTTCCACCGTCTCAG 1500
Qy 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524
Db 1501 CAGTCTCCGAGGCTGTGGCTTAA 1524

RESULT 7

US-10-958-324-4
; Sequence 4, Application US/10958324
; Publication No. US20050114924A1
; GENERAL INFORMATION:
; APPLICANT: DODO, HORTENSE W.
; APPLICANT: ARNTZEN, CHARLES J.
; APPLICANT: KONAN, KOFFI N'DA
; APPLICANT: VIQUEZ, OLGA
; TITLE OF INVENTION: DOWN-REGULATION AND SILENCING OF ALLERGEN GENES IN
; FILE OF INVENTION: TRANSGENIC PEANUT SEEDS
; FILE REFERENCE: 072121/0104
; CURRENT APPLICATION NUMBER: US/10/958,324
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/715,036
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/167,255
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Arachis hypogaea
US-10-958-324-4

Query Match 91.3%; Score 1391.2; DB 10; Length 1853;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 68; Indels 2; Gaps 2;
Qy 2 GGCAGCAACCGGAGGAAACGCGTCCAGTTCAGCGCCTCAATGGCAGACCTTGACA 61
Db 71 GGCAGCAGCCGGAGGAATGCGTGCCAGTTCAGCGCCTCAATGGCAGACCTTGACA 130
Qy 62 ATCGCATTTGAATCAGAGGGGGTTACATTCAGACTTGGAAACCCCAACCAACAGGATTCG 121
Db 131 ACCGATTTGAATCGGAGGGGGTTACATTCAGACTTGGAAACCCCAACCAACAGGATTCG 190
Qy 122 AATGCGCGCGCGTCCGCTCTCTCGTTAGTCTCTCGCGCCCAACGCCCTTCGTAGGCCCT 181
Db 191 AATGCGCGCGCGTCCGCTCTCTCGTTAGTCTCTCGCGCCCAACGCCCTTCGTAGGCCCT 250
Qy 182 TCTACTCCAATGTCCTCCAGAGATCTTCAATTCAGCAGAGGAGGATCTTTGGGTGA 241
Db 251 TCTACTCCAATGTCCTCCAGAGATCTTCAATTCAGCAGAGGAGGATCTTTGGGTGA 310
Qy 242 TATTCCCTGCTGCTCTAGACATATGAGAGGCTCACACAGGCTCGTCTGATCTCAGT 301
Db 311 TATTCCCTGCTGCTCTAGACATATGAGAGGCTCGTCAACAGGAGGAGGATCTCAGT 370
Qy 302 CCCAAGACCAACCAAGAGCTCTCAAGAGAGAGACCAAGGCCCAACAGCAACGAGATGTC 361
Db 371 CCCAAGACCAACCAAGAGCTTTCAGAGAGAGACCAAGGCCCAACAGCAACGAGATGTC 430
Qy 362 ACCAAGAGGTGCACCGTTTCAGTGGGGTATCTCATTCAGTTCCTCCACCGGTGTCCT 421
Db 431 ACCAAGAGGTGCACCGTTTCAGTGGGGTATCTCATTCAGTTCCTCCACCGGTGTCCT 490

Qy 422 TCTGGCTCTACACGACGACGACACTGATGTTGTTGCTGTTTCTCTTACTGACACCAACA 481
Db 491 TCTGGCTGTACACGACGACGACACTGATGTTGTTGCTGTTTCTCTTACTGACACCAACA 550
Qy 482 ACAAAGCAACGAGCTTGATCAGTCCCAAGGAGATTCAAATTTGGCTGGGAACAGGAGC 541
Db 551 ACAAAGCAACGAGCTTGATCAGTCCCAAGGAGATTCAAATTTGGCTGGGAACAGGAGC 610
Qy 542 AAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGCAAGAAAGCTTACCATATA 601
Db 611 AAGAGTTCTTAAGGTACCAGCAACAAAGCAGACAAAGCAGCAAGAAAGCTTACCATATA 670
Qy 602 GCCCATACAGCCCGCAAGTCAAGTACAGCAAGAGAGCGTGAATTTAGCCCTCGAGGAC 661
Db 671 GCCCATACAGCCCGCATAGTCCGCTTAGACAGAGAGCGTGAATTTTCGCCCTCGAGGAC 730
Qy 662 AGCAGAGCCGACAGAGAACGAGGAGGACAGAGAAAGAAAGAAAGGTTGGAACATCTTCA 721
Db 731 AGCAGAGCCGACAGAGAACGAGGAGGACAGAGAAAGAAAGAAAGGTTGGAACATCTTCA 790
Qy 722 GCGGCTTCAGCCGAGTTCCTCGAAACAGCTTCAGGTTGAGCAGACAGATAGTGC 781
Db 791 GCGGCTTCAGCCGAGTTCCTCGAAACAGCTTCAGGTTGAGCAGACAGATAGTGC 850
Qy 782 AAAACCTTAAGAGCGAGACCGAGAGTGAAGAGGAGGAGCCATTGTGACAGTGAAGGAG 841
Db 851 AAAATCTGTGGGCGAGAGCGAGTGAAGAGGAGGAGCCATTGTGACGTTGAGGAGGAG 910
Qy 842 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGCGTCCGACGAGAGAGAAATACGATG 901
Db 911 GCCTCAGAAATCTTGAAGCCAGATAGAAAGAGAGTCCGACGAGAGAGAAATACGATG 970
Qy 902 AAGATCAATATGAATACGATGAAGAGATAGAGGCGTGCAGGGAAGCAGAGGAGGAGG 961
Db 971 AAGATCAATATGAATACGATGAAGAGGCGTGCAGGGAAGCAGAGGAGGAGGAGG 1030
Qy 962 GGAATGTTTGAAGAGAGAGATCTGCACCGCAAGTCTAAAAAGAAACATTTGGTAGAAACA 1021
Db 1031 GGAATGTTTGAAGAGAGAGATCTGCACCGCATGTGTTAAAAAGAAACATTTGGTAGAAACA 1090
Qy 1022 GATCCCTGACATCTACACCTCA - AGCTGGTTCACTCAAAACTGCAACGATCTCAAC 1080
Db 1091 GATCCCTGACATCTACGATCTCAGCGTGGTTCACTCAAAACTGCAACGATCTCAAC 1149
Qy 1081 CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGAAATGCA 1140
Db 1150 CTTCTAATCTTAGTGGCTTGGACCTAGTCTGAAATATGAAATCTCTACAGAAATGCA 1209
Qy 1141 TTCTTTTGTGGCTCACTACAAACCAACGACACAGCATCATATATCGATTGAGGGAGCGG 1200
Db 1210 TTGTTTGTCCCTCACTACAAACCAACGACACAGCATCATATATGCAATTGAGGGAGCGG 1269
Qy 1201 GCTCAGTGAAGTCTGTGACAGCAACGCGCAACAGAGTGTACAGAGGAGCTTCAAGAG 1260
Db 1270 GCTCAGTGAAGTGTGACAGCAACGCGCAACAGAGTGTACAGAGGAGCTTCAAGAG 1329
Qy 1261 GGTACAGTGTGTTGGTGCACAGAACTTCGCGCTGCTGGAAGTCCAGAGGAGAGAAC 1320
Db 1330 GGTACAGTGTGTTGGTGCACAGAACTTCGCGCTGCTGGAAGTCCAGAGGAGAGAAC 1389
Qy 1321 TTGGAATACGTGGCATTTCAAGCAGACTCAAGGCCAGAGATAGCCAACTTCGCGGTGAA 1380
Db 1390 TTGGAATACGTGGCATTTCAAGCAGACTCAAGGCCAGAGATAGCCAACTTTGCGGTGAA 1449
Qy 1381 AACTCCGTATAGATAACCTGCGGAGGAGTGGTTGCAAAATTCATATGCGCTCCAAAGG 1440
Db 1450 AACTCCGTATAGATAACCTGCGGAGGAGTGGTTGCAAAATTCATATGCGCTCCCAAGG 1509
Qy 1441 GAGCAGGAGGAGCTTAAGAACAAACCCCTTCAAGTTCCTCGTTCACCGCTCTCAG 1500
Db 1510 GAGCAGGAGGAGCTTAAGAACAAACCCCTTCAAGTTCCTCGTTCACCGCTCTCAG 1569

QY 1501 CAGTCTCCGAGGCGTGTGGCTTAA 1524
Db |||||
1570 CAGTCTCCGAGGCGTGTGGCTTAA 1593

RESULT 8

US-09-758-652-13
; Sequence 13, Application US/09758652
; Patent No. US20010011377A1
; GENERAL INFORMATION:
; APPLICANT: ANTHONY JOHN KINNEY
; GARY MICHAEL FADER
; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC
; CLASSES OF SOYBEAN SEED
; PROTEIN GENES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,652
; FILING DATE: 11-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/019,940
; FILING DATE: JUNE 14,1996
; ATTORNEY/AGENT INFORMATION:
; NAME: LYNNE M. CHRISTENBURY
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: BB-1071-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-5481
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-758-652-13

Query Match 34.0%; Score 517.4; DB 3; Length 1446;
Best Local Similarity 62.8%; Pred. No. 3.2e-154;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY 5 AGCAACGGGAGAGCGCTGCAGTTCAGCGCCTCAATGCGCAGAGACCTGACAATC 64
Db |||||
71 AGCAGCCACAGCAAAACGAGTGCAGATCCAAACGCTCAATGCCCTTAAACCGGATAAC 130
QY 65 GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAAACCCCAACCAACGAGGTTGGAAT 124
Db 131 GTATAGATCAGAGGTGGCTTCATTGAGCATGGAACCTTAACAACAGCCATTCCAGT 190
QY 125 GCGCCGGCGTGCCTCTCTCGCTTAGTCTCCGCGCGCAACGCGCCTTGGTAGCCTTTCT 184
Db 191 GTGCGCGTGTGCGCTCTCTCGCTGACCTCAACCGCAACGCGCTTTCGACAGCCTTCT 250
QY 185 ACTCCATGCTCCCGAGGAGATCTTCATCCAGCAAGGAGGGGATATCTTTGGGTGTATAT 244
Db 251 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGGTATTTTGGCATGATAT 310
QY 245 TCCTCGTTGTCTCTAGACACTATGAGAGCGCTCACACAAAGGTGCTGATCTCAGTCCC 304

Db |||||
311 TCCCGGTTGTCTTAGCACATTTGAAGAGCCT----- 342
QY 305 AAAGACCACCAAGACGTCTCCAAGGAGAACCAAGCCAAACAGCAACGAGATAGTACCC 364
Db |||||
343 -----CAACAAAAGGACAAAGCAGCAGCGGCCCAAGACCGTACCC 382
QY 365 AGAAGGTGACACCGTTTCGATGAGGGTGATCTCATTCAGTTCGCCCGGTGTTGCTTTCT 424
Db |||||
383 AGAAGATCTATCATTTCAGAGAGGGTGATTGATTCAGTGCCCAACCGGTTTGCATACT 442
QY 425 GGCTCTCAACACGACCAACGACACTGATGTTGCTGCTGTTCTCTTACTGACACCAACACA 484
Db |||||
443 GGATGTACAAACAATGAAGACACTCTCTGTTGTTGCGCTTTCTCTTATTGACACCAACAGCT 502
QY 485 ACGACAACCGAGCTTGATCAGTTCCTCCAGGAGATTCATTTGGCTGGGAACCGGAGCAAG 544
Db |||||
503 TCAGAACCCAGCTTCGACCCAGATGCTCTAGGAGATTCTATCTTGTGGGAACCAAGAGCAAG 562
QY 545 AGTTCTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACGAAAGCTTACCATATAGCC 604
Db |||||
563 AGTTCTTACAGTATCAGCCACAGACGACGCAAG----- 595
QY 605 CATACAGCCGCAAGTTCAGCCTTAGACAAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
Db |||||
596 -----GAGGTACTC 604
QY 665 ACAGCCGACAGAACGACGAGGACAGAAAGAAACGAAAGGTGGAACATCTTCAGCG 724
Db |||||
605 AAAGCCAGAAAGGAAAGCGTTCAGAGAAAGAAACGAAAGGAGCGCATTTAGTG 664
QY 725 GCTTACAGCGCGGAGTTCTTGGAAACAGCCTTCAGGTTGACGACAGACAGATAGTCAAA 784
Db |||||
665 GCTTCCCGCGGNAATCTTGGACATGCGCTTC---GTCGTGGACAGCAGATAGTGAA 721
QY 785 ACCTAAGAGCGAGACCGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGGAGGCC 844
Db |||||
722 AGCTCAAGGTGAGAAACGAAAGAGAGAGGAGGAGGAGGTCATTGTGACAGTGAAGAGGAGTC 781
QY 845 TCAGAACTTGGAGCCAGATAGAAAGAGAGCGTCCGACGAAAGAGAGGAAATACGATGAAG 904
Db |||||
782 TCAGCGTGATAGGCCACCCACCGAAGAGCAGCAACAAAGACCCGAGGAAAGAGAGAGC 841
QY 905 ATGAATATGAATACGATGAAGAGGATAGAAGCGGTGGCAGGGGAAAGCAGAGCGAGGGA 964
Db |||||
842 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA 886
QY 965 ATGGTATTGAAGAGAGCATCTGCACCGCAAGTCTCTAAAAGAACATTGTTAGAAACAGAT 1024
Db |||||
887 ATGGCATTTGACGAGACCATTTGCACAAATGAGACTTCGCCCAACATTTGGCCAGACTTCAT 946
QY 1025 CCCTGACATCTACAAACCTCAAGCTGGTTTCACTCAAAACCTGCCAACGATCTCAACCTTC 1084
Db |||||
947 CAGCTGACATCTTCAACCTTCAAGCTGGTAGCATCAACCGGTACCGCTCGACTTCC 1006
QY 1085 TAATACCTTAGGTGGCTTGGACCTTAGTCTGAAATATGAAATCTCTACAGAAATGCAATTGT 1144
Db |||||
1007 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCAGTTTGGATCACTCCGCAAGAAATGCTATGT 1066
QY 1145 TTGTCGCTCATCAACACCAACGCAACAGCATCATATATATTCGATTGAGGGGAGCGGCTC 1204
Db |||||
1067 TCGTGCCACACTACAAACCTGAAACGCAACAGCATATATACGCAATTTGAATGGAGCGGCAT 1126
QY 1205 ACCTGCAAGTCTGGGACAGCAACGCAACAGAGTGACGACGAGGAGCTTCAAGAGGGTC 1264
Db |||||
1127 TGGTACAAAGTGGTGAATTCGATGAGAGAGTGTGTTGATGGAGAGCTCAAGAGGGAC 1186
QY 1265 ACCTGCTTGTGGTCCACAGAACTTCGCGCTCGCTGAAAGTCCAGAGAGCAACTTCG 1324
Db |||||
1187 AGGTGTTAATTTGTGCCACAAAACCTTTGCGGTGGCTGCAAGATCACAGAGCGCAACTTCG 1246
QY 1325 AATACGTGGCATTTCAAGACAGACTCAGGGCCAGCATAGCAACCTCGCGGTGAAACT 1384
Db |||||

Db 1067 TCGTGCCACACTACAACTGAACGCAACAGCATATATACGCATTGAATGAGCGGCAT 1126
QY 1205 AGTGCAAGTCGTGGACAGCAACAGCGCAACAGAGTGTACAGAGGAGCTTCAAGAGGGTC 1264
Db 1127 TGGTACAAGTGGTGAATTCGAATGGTGTGAGAGAGTGTGTGATGGAGAGCTGCAAGAGGGAC 1186
QY 1265 AGTGCTTGTGGTCCACAGAACTTCGCGTGTGCTGCTGGAAGTCCACAGAGCGAAGCTTCG 1324
Db 1187 AGTGTTAATTGTGCCACAAAACCTTTCGGTGGCTGCAAGATCACAGAGCGACAACCTTCG 1246
QY 1325 AATACGTGCATTCAAGACAGACTCAAGGCCAGCATAGCCAACTTCGCGGTGAAAACT 1384
Db 1247 AGTATGTTTCATTCAAGACCAATGATAGACCCTCGATCGCAACCTTGCAGGTGCAAACT 1306
QY 1385 CGGTATAGATAACCTGCGCGAGGAGTGGTGTGCAAAATTCATATGCGCTCCAAAGGGAGC 1444
Db 1307 CATTTGTAACGCAATTCGCGGAGGAAGTGAATTCAGCAAACTTTTAACTTAAGGAGGCGC 1366
QY 1445 AGCAGGAGGAGCTTAAGAACAAACCCCTTCAAGTTCCTTCCACCGTCTCAGCAGT 1504
Db 1367 AGCCAGGAGGAGTCAAGAACAAACCCCTTTCAGTTCCTGTTCCACCTTAAGGAGTCTC 1426
QY 1505 CTCGAGGAGGCTGTGGCTTA 1523
Db 1427 AGAGGAGAGTGTGGCTTA 1445

RESULT 10

US-10-757-074-13

; Sequence 13, Application US/10757074

; Publication No. US20040139502A1

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10757,074

; FILING DATE: 14-Jan-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/758,652

; FILING DATE: 11-Jan-2001

; APPLICATION NUMBER: 60/019,940

; FILING DATE: JUNE 14,1996

; ATTORNEY/AGENT INFORMATION:

; NAME: LYNNE M. CHRISTENBURY

; REGISTRATION NUMBER: 30,971

; REFERENCE/DOCKET NUMBER: BB-1071-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-992-5481

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1446 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-757-074-13

Query Match 34.0%; Score 517.4; DB 8; Length 1446;

Best Local Similarity 62.8%; Pred. No. 3.2e-154;

Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY	5	AGCAACCGGAGAGACGCGTCCAGTTCACGCGCTCAATGCGGAGAGACCTTGACAATC	64
Db	71	AGAGCCACAGCAAAACAGAGTCCAGATCCAGCCTCAATGCCCTTAAACCGGATPACC	130
QY	65	GCATTGAATCAGAGGCGGTTTACATTGAGACTTGGAAACCCCAACAAACAGGAGTTGCAAT	124
Db	131	GTATAGAGTCAGAGGTGCTTCATTGAGACATGGAACCTTAACAACAGCCATTCCAGT	190
QY	125	GGCCGGCGTCCGCTCTCTCGCTTAGTCTCTCGCGCGAAACGCGCTTCGTAGGCGTTTCT	184
Db	191	GTGCGGCTTGTGCGCTCTCTCGCTGACCCCTCAACCGCAACGCGCTTCGACAGACCTTCT	250
QY	185	ACTCCAATGCTCCAGGAGATCTTCATCCAGCAAGGAAGGGGATACTTTGGTTGATAT	244
Db	251	ACACCAACGCTCCCGAGGAGATCTCATCCAAAGGTAGTGGTATTTTGGCATGATAT	310
QY	245	TCCCTGGTTGTCTTAGACACTATGAGAGCCTCACACAAAGTCTCGATCTCAGTCCC	304
Db	311	TCCCGGTTGTCTTAGACACTTTGAAGACCT-----	342
QY	305	AAAGACCAAGACGCTCTCAAGGAGAGAACCAAGCCAAACAGCAACAGATAGTCACC	364
Db	343	-----CAACAAAAGGACAAAGCAGAGCGGCCCAAGACCGTCACC	382
QY	365	AGAAGGTGCACCGTTTCGATGAGGTGATCTCATTCAGTTCGCCACCGTGTGCTTCT	424
Db	383	AGAAGATCTATCATTACAGAGAGGTGATTTGATTCAGTGCACACCGTGTGCTACT	442
QY	425	GGCTCTAACACGACCACTGATGTTGTTGCTGTTCTCTTACTGACACCAACAA	484
Db	443	GGATGTACAAACATGAAGACACTCCTGTTGTTGCGCTTCTCTTATTGACACCAACAGCT	502
QY	485	AGCAACACAGCTTGATCAGTTCGCCAGAGATTCAATTTGGCTGGAAACACGAGCAAG	544
Db	503	TCCAGAACCAAGTCCGACAGATGCTTAGGAGATTCTATCTTGCTGGGAACCAAGCAAG	562
QY	545	AGTTCTTAAGGTACCAAGCAACAAAGCAGACAAAGCAGACGAAGAGCTTACCATATAGCC	604
Db	563	AGTTCTTACAGTATCAGCCACAGACGACGCAAG-----	595
QY	605	CATACAGCCCGCAAGTTCAGCTTAGACAAAGAGAGCGTGAATTTAGCCCTCGAGGACAGC	664
Db	596	-----GAGGTACTC	604
QY	665	ACGCCGAGAGAACGAGCAGGACAGCAAGAAACGAGGTGGAAACATCTTCAGCG	724
Db	605	AAAGCCAGAAAGGAAAGCGTCAGCAAGAGAGAAACGAGGAGGAGCATATTGAGTG	664
QY	725	GCTTACAGCGGAGTTCTCGGAAACAGCTTCCAGGTTCACGACAGACAGATAGTCAAA	784
Db	665	GCTTCCCGCGGAATCTTGGAAACATGCGTTC---GTCTGGACAGCAGATAGTGAGAA	721
QY	785	ACCTAAGAGCGAGACCGGAGGTGAAGAAAGAGGAGCCATTGTGACAGTAGGGGAGGCC	844
Db	722	AGCTACAGGTGAGAACGAAGAGGAGAGAGGGTGCATTTGTGACAGTGAAGAGGAGTGC	781
QY	845	TCAGAACTTTAGCCCCAGATAGAAAGAGAGCTGCCCGACGAGAGAGGAGATACGATGAAG	904
Db	782	TCAGCGTGATAGCCCCACCCACCGAAGAGCAGCAACAAAGACCCGAGGAAAGAGAGAAC	841
QY	905	ATCAATATGAATACGATGAAGAGGATAGAAGGCGTGGCAGGGGAAGCAGAGGAGGGGGA	964
Db	842	CAGATTGTGACGAGAAAGCAAACT-----TGCCAAAGCCAAAGCAGAA	886
QY	965	ATGTTATTGAAGAGACGATCTGCACCGCAAGTCTTAAAGAACATTGTGTAGAAACAGAT	1024

Db 887 ATGGCATTGAGGAGCAATTTGCAATGAGACTTCCGCCACAACATTTGGCCAGACTTTCAT 946
QY 1025 CCCTGACATCTAACACCCCTCAAGCTGGTTCACTCAAAACTGGCCAAAGATCTCAACCTTC 1084
Db 947 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACCGCTACCAGCTCGACTTCC 1006
QY 1085 TAATACCTAGTGGCTTGGAGCTAGTGTCTGAATATGGAATCTCTACAGGAATGCAATGT 1144
Db 1007 CAGCCCTCTCGTGGCTCAAACTCAGTGTCCAGTTTGGATCACTCCGCAAGAATGCTATGT 1066
QY 1145 TTGTGCTCTACTAACACCAACCGCACACAGCATCATATATCGATTGAGGGGAGCGGCTC 1204
Db 1067 TCGTGCCACACTCAACCTGACGCAACAGCATATATAGCATTGAATGGACGGGCAT 1126
QY 1205 ACCTGCAAGTGTGGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264
Db 1127 TGGTACAAGTGGTGAATTGCAATGGTGAGAGAGTGTGATGAGAGCTGCAAGAGGGAC 1186
QY 1265 ACCTGCTTGTGGTGGCACAGAACTTGGCGTGGTGAAGTCCGAGAGGAGAACTTCG 1324
Db 1187 AGGTGTAAATTGTGCCACAAACTTTGCGGTGGTGCAGATCACAGAGCGCAAACTTCG 1246
QY 1325 AATACGTGGCATTCAAGACAGACTCAAGGCCAGCATAGCCACCTCGCGGTGAAACT 1384
Db 1247 AGTATGTTTCATTCAAGACCAATGATAGACCTCGATCGCAACCTTGCAGGTGCAAACT 1306
QY 1385 CCCTCATAGATAACCTCGCGGAGGAGTGTGCAAAATTCATATGGCTCCAAAGGAGC 1444
Db 1307 CATTGTTGAACGATTGCGGAGGAGTGTATCAGCAAACTTTTAACCTAAGAGGCGAGC 1366
QY 1445 AGCAAGGCGAGTTAAGAACAAACACCCCTTCAAGTTCTTTCGTTCCACCGTCTCAGCAGT 1504
Db 1367 AGCCAGGCGAGTCAAGAACCAACACCCCTTTCAGCTTCTCGTTCCACCTAAGGAGTCTC 1426
QY 1505 CTCGAGGCGTGTGGCTTA 1523
Db 1427 AGAGGAGGTTGTGGCTTA 1445

RESULT 11

US-10-757-155-13

; Sequence 13, Application US/10757155

; Publication No. US20040139503A1

; GENERAL INFORMATION:

; APPLICANT: ANTHONY JOHN KINNEY

; GARY MICHAEL FADER

; TITLE OF INVENTION: SUPPRESSION OF SPECIFIC

; CLASSES OF SOYBEAN SEED

; PROTEIN GENES

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

; STREET: 1007 MARKET STREET

; CITY: WILMINGTON

; STATE: DELAWARE

; COUNTRY: UNITED STATES OF AMERICA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 INCH

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MICROSOFT WINDOWS 95

; SOFTWARE: MICROSOFT WORD 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10757,155

; FILING DATE: 14-Jan-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/758,652

; FILING DATE: 11-Jan-2001

; APPLICATION NUMBER: 60/019,940

; FILING DATE: JUNE 14,1996

; ATTORNEY/AGENT INFORMATION:

; NAME: LYNNE M. CHRISTENBURY

; REGISTRATION NUMBER: 30,971

; REFERENCE/DOCKET NUMBER: BB-1071-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 302-992-5481

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1446 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 13:

; US-10-757-155-13

Query Match 34.0%; Score 517.4; DB 8; Length 1446;

Best Local Similarity 62.8%; Pred. No. 3.2e-154; Indels 144; Gaps 4;

Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY 5 AGCAACCGGAGGAGAACGCGTGCAGTTCAGGCGCTCAATGCGCAGAGACTTGCACATC 64

Db 71 AGCAGCCACAGCAAAACGAGTGCAGATCCACGCTCAATGCCCTAAACCGGATAACC 130

QY 65 GCATTGAATCAGAGGGGGTTACATTTGAGACTTGGAAACCCCAACACAGAGTTTGAAT 124

Db 131 GTATAGAGTCAGAAGGTGGCTTCATTGAGACATGGAACCCCTAAACCAAGCCATTCCAGT 190

QY 125 GCGCCGCGTGCCTCTCTCGCTTAGTCCCTCGCGCACGCGCTTCTCGTAGGCTTTCT 184

Db 191 GTCCCGGTGTGCTCTCTCGCTGACCCCTCAACCGCACGCTTTCGAGAGCTTCTCT 250

QY 185 ACTCCAAATGTCTCCAGGAGATCTTCATCCAGCAAGGAAGGGATCTTTGGGTGATAT 244

Db 251 ACACCAACGCTCCCGAGGAGATCTACATCAACAGGTAGTGTATTTTGGCATGATAT 310

QY 245 TCCCTGGTTGCTCTAGACACTATGAAGAGCCTCACACAAAGGTGCTGATCTCAGTCCC 304

Db 311 TCCCGGTGTGCTCTAGCACATTTGAAGAGCCT----- 342

QY 305 AAAGACCACCAAGACGCTCTCAGGAGAGAACCAAGCCAAACAGAACGAGATAGTACCC 364

Db 343 -----CAACAAAAGGACAAAGACGAGCGCCCAAGACGCTCACC 382

QY 365 AGAAGGTGACCCGTTTCGATGAGGGTGATCTCATTTGAGTTCACCGGTGCTGCTTCT 424

Db 383 AGAAGATCTATCACTTCAGAGAGGGTGATTGATTGAGTGCACCGGTTCGATACT 442

QY 425 GGCTCTACAAACGACACGACACTGATGTTGTTGCTGTTCTTACTGACACCAACAA 484

Db 443 GGATGTACAAACAAATGAAGACACTCTCTGTTGTCGCTTTCTTTATTTGACCAACAGCT 502

QY 485 ACACAAACGAGCTTGATCAGTTCCCGAGGAGATTCAATTTGGCTGGGAACCGGACGAG 544

Db 503 TCCAGAACGAGCTCGACCAAGTGCCTAGGAGATTCTATCTTCTGGGAACCAAGAGCAAG 562

QY 545 AGTTCTTAAGGTACACAGCAACAAAGACAGACAAAGAGAGCTTACCATATAGCC 604

Db 563 AGTTCTACAGTATCAGCCACAGACGACGAG----- 595

QY 605 CATAAGCCCGCAAGTTCAGCTTAGACAAAGAGAGCGTGAATTTAGCCCTTCGAGGACAG 664

Db 596 -----GAGGTACTC 604

QY 665 ACAGCCGAGAGAACGAGCAGGACAGAAAGAAACGAGGTGGAACATCTTCAGCG 724

Db 605 AAAGCCAGAAAGGAAAGCGCTCAGCAAGAAAGAAACGAGGAGGACGATATTGAGTG 664

QY 725 GCTTACGCGGAGTTCTTGGAAACAGCTTCCAGGTTGACGACACAGATAGTCAAA 784

Db 665 GCTTCCCGCGGAATCTTGGAAACATCGCTTC---GTCTGGACAGGACAGATAGTGAA 721

QY 785 ACCTAAGAGCGAGACCGGAGAGTGAAGAGAGGAGGCCATTTGTACAGTGTAGGGAGGCC 844

596 -----GAGGTACTC 604
Db
QY 665 ACAGCCGAGAGAACGAGCAGGACAAAGAAAGAAACGAGGTGGAAACATCTTCAGCG 724
Db
QY 605 AAAGCCAGAAAGAAAGGTCAGCAAGAGAAAGAAAGAAAGAGGAGGAGCAGCATATGAGTG 664
QY 725 GCTTCAAGCCGAGGATTCCTGGAAACAGCCTTCCAGGTGACGACAGATAGTGCAAA 784
Db
QY 665 GCTTCGCCCGGAAATCTTGGAAACATCGCTTC---GTCTGGACAGGACAGATAGTGA 721
QY 785 ACCTAAGAGCGGACGAGCAGGAGTGAAGNAGGAGGAGCATTTGACAGTGAAGGGAGGCC 844
Db
QY 722 AGCTACAGGTGAAGCAAGAGAGAGAGAGAGGAGGAGGAGTGTGACAGTGAAGAGGTC 781
QY 845 TCAGAAATCTTGAAGCCAGATAGAAAGAGAGAGTGCAGGAGAGAGAGAGATACATCAAG 904
Db
QY 782 TCAGCGTGATAGCCACCCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 841
QY 905 ATGATATGATAGATGAGAGAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 964
Db
QY 842 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA 886
QY 965 ATGATATGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1024
Db
QY 887 ATGATATGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 946
QY 1025 CCCTGACATCTCAACCCCTCAAGCTGTTTCACTCAAAAGCTGCAAGAGATCTCAACCTTC 1084
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QY 947 CACTGACATCTCAACCCCTCAAGCTGTTTCACTCAAAAGCTGCAAGAGATCTCAACCTTC 1006
QY 1085 TAATATCTAGGTGGCTTGGACCTAGTGTCTGAATATGAAATCTCTACAGGAATGCAATGT 1144
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QY 1007 CAGCCCTCTCGTGGCTCAAACTCAGTGTCCAGTTTGGATCACTCCGCAAGATGCTATGT 1066
QY 1145 TTGTCGCTCACTCAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1204
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QY 1067 TCGTGCCACTCAACCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1126
QY 1205 ACCTGCAAGTCTGGAGCAGCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1264
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QY 1127 TGATCAAGTGGTGAATGCAATGCTGAGAGAGTGTGATGAGAGAGTCTCAAGAGGAGC 1186
QY 1265 ACCTGCTTGTGGTGCACAGAACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
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QY 1187 AGGTGTTAAATGTCGACAAACTTTGCGGTGCTGCAAGATCACAGAGCGCAACTTCG 1246
QY 1325 AATACGTGGCATTCAGACAGACTCAAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1384
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QY 1247 AGTATGTTTCAATCAAGACCAATGATAGACCTCGATCGGCAACCTTGCAGGTGCAACT 1306
QY 1385 CCGTCATAGATAACCTGCGGAGGAGTGTGCAAAATTCATATGGCTCCAAAGGAGC 1444
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QY 1307 CATTTGTGAACGATTTGCGGAGAGAGTGTGATGAGAGAGTGTGATGAGAGAGCAGC 1366
QY 1445 AGCAAGGAGCTTAAGAAACAAACCCCTTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTG 1504
Db
QY 1367 AGCCAGGAGGTCAGAAACAAACCCCTTCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTG 1426
QY 1505 CTCGAGGAGTGTGGCTTA 1523
Db 1427 AGAGGAGAGTGTGGCTTA 1445

RESULT 13

US-10-508-263-27
; Sequence 27, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Constructs and methods for regulating gene expression
; FILE REFERENCE: 53262-20085.00
; CURRENT APPLICATION NUMBER: US/10/508, 263
; CURRENT FILING DATE: 2004-09-20

; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1443)
; OTHER INFORMATION: glycinin G3 subunit
US-10-508-263-27

Query Match 34.0%; Score 517.4; DB 10; Length 1446;

Best Local Similarity 62.8%; Pred. No. 3.2e-154;

Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

QY 5 AGCAACCGAGAGGAGAACGCGTGCAGGTTCCAGCGCTCAATTCGCGAGAGACTGACAAATC 64
Db 71 AGCAGCCACAGCAAAACGAGTGCCAGATCCAAACGCTCAATGCTTAAACCGGATACC 130
QY 65 GCATTGAATCAGAGGCGGTTACATTTGAGACTTTGGAACCCCAACACGAGGTTCCGAAT 124
Db 131 GTATAGAGTCAGAAAGTGGCTTCATTGAGACATGGAACCCCTTAAACAAGCCATTCAGT 190
QY 125 GCACCGCGCTCGCCCTCTCTCGCTTAGTCTCGCCGCAACGCTTCGTAGGCTTTCT 184
Db 191 GTCCGCTGTTCCTCTCTCGCTGCACCTCAACCGCAACGCTTCGCGAGACTTCT 250
QY 185 ACTCCAATGTCCTCCAGGAGATCTTATCCAGCAAGAAAGGGATATCTTTGGGTGATAT 244
Db 251 ACACCAACGCTCCCGAGGAGATCTACATCCAAAGGTAGTGGTATTTTGGCATGATAT 310
QY 245 TCCTGCTGCTCTAGACATATGAAGAGCTTCACACACAAGGTCGTGATCTCAGTCCC 304
Db 311 TCCGCGTGTCTAGACATTTGAAGGCT----- 342
QY 305 AAAGACCAACCAAGCGCTCTCAAGAGAGAGACCAAGCAACAGCAACGAGATAGTCAAC 364
Db 343 -----CAACAAAGAGCAAAAGCAGCAGGCGCCCAAGCGTCAAC 382
QY 365 AGAAGTGCAACCGTTTCGATGAGGGTGATCTCATTTGAGTTCCACCGGTGTTCTTCT 424
Db 383 AGAAGATCTATCACTTCAGAGAGGTTGATTTGATTTGAGTGCACCAACCGGTTTGCATAC 442
QY 425 GGCTCTACAAACGACGACGACACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 484
Db 443 GGATGTACAAATGAAGACACTCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 502
QY 485 ACACAAACGAGCTTGATCAGTTCCCGAGGAGATTCAATTTGGCTGGGAACACGAGGCAAG 544
Db 503 TCCAGAAACGAGCTCGACAGATGCTTAGGAGATTCTATCTTGTGGGAACCAAGAGCAAG 562
QY 545 AGTTCTTAAGGTACAGCAACAAAGCAGACAAAGCAGACAAAGCAGACGAAGAGCTTACCATATAGCC 604
Db 563 AGTTCTTACAGTATCAGCCACAGAGCAGCAAG- 595
QY 605 CATACAGCCGCAAAAGTGCAGCTAGACAAAGAGCGTGAATTTAGCCCTCGAGGACAGC 664
Db 596 -----GAGGTACTC 604
QY 665 ACAGCCGAGAGAAACGAGCAGGACAAAGAAAGAAACGAGGTGGAAACATCTTCAGCG 724
Db 605 AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAAGAAAGGAGGAGCAGCATATGAGTG 664
QY 725 GCTTACGCGGAGTTCTTGGAAACAGCCTTCAGGTTGACGACAGACAGATAGTGCAAA 784
Db 665 GCTTCGCCCGGAAATCTTGGAAACATGCGCTTC---GTCTGGACAGGACAGATAGTGA 721
QY 785 ACCTAAGAGCGCAGACCGGAGAGTGAAGAGAGAGGAGGCCATTTGTGACAGTGAAGGGAGGCC 844
Db 722 AGCTCAAGGTGAGAAACAGAGAGAGAGAGAGGAGGTCCTTGTGACAGTGAAGAGGAGTGC 781
QY 845 TCAGAAATCTTGAGCCCAAGATAGAAAGAGAGAGCTGCCGAGAGAGAGGAGGATACGATGAAG 904

Db 969 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCAACACCGTACCAGCCTCGACTTCC 1028
Qy 1085 TAATACCTAGGTGGCTTGGACCTAGTCTGAATATGGAATCTCTACAGGAATGCAATGT 1144
Db 1029 CAGCCCTCTCGTGGCTCAAACTCAGTGGCCAGTTGGATCACTCCGCAAGAATGCTATGT 1088
Qy 1145 TTGTGCTCACTACAACCAACAGGCACACAGCATCATATATCATATGATGAGGGGACGGGCTC 1204
Db 1089 TCGTGCCACACTACAACCTGAACGCAACAGCAATATATACGCATTGAATGGACGGGCAT 1148
Qy 1205 ACGTGAAGTCGTGGACAGCAACGGCAACAGATGTACGAGGAGCTTCAAGAGGGTC 1264
Db 1149 TGGTACAAGTGGTGAATTTGCAATGGTGAGAGAGTGTGTTGATGGAGAGCTGCAAGAGGGAC 1208
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Db 1209 AGGTGTTAATGTGGCCCAAACTTTTCGGTGGCTGCAAGATCACAGAGGCAACTTCG 1268
Qy 1325 AATACGTGGCAITCAAGACAGACTCAAGGCCAGCATAGCCAACTCGCGGTGAAACT 1384
Db 1269 AGTATGTTTCAATCAAGACCAATGATAGACCTCGATCGGCACTTGCAGGTGCAACT 1328
Qy 1385 CCGTCATAGATAACCTCCCGGAGAGGTGTGCGAAATTCATATGGCTTCAAAAGGAGC 1444
Db 1329 CATTGTTGAACGCAATTCGCGGAGGAGTGAATTCAGCAAACTTTTAACCTAAGGAGGAGC 1388
Qy 1445 AGCGAGGAGCTTAGAACAACACCCCTTCAAGTTCTTCGTTCCACCGTCTCAGCAGT 1504
Db 1389 AGCCAGGAGGAGTCAAGAACAAACCCCTTTCAGCTTCCTGGTTCCACCTAAGAGGTCTC 1448
Qy 1505 CTCGAGGGCTGTGGCTTA 1523
Db 1449 AGAGGAGGTGTGGCTTA 1467

RESULT 15

US-10-425-114-8531
; Sequence 8531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 8531
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700757865_FLI
US-10-425-114-8531

Query Match 34.0%; Score 517.4; DB 8; Length 1689;
Best Local Similarity 62.8%; Pred. No. 3.4e-154;
Matches 954; Conservative 0; Mismatches 421; Indels 144; Gaps 4;

Qy 5 AGCAACGGAGGAGAACGCTGCGAGTTCAGGCGCTCAATGGCGAGACCTGACAATC 64
Db 105 AGCAGCCACAGCAAAACGAGTGCAGATCCAAAGCGCTCAATGCCCTCAAAACCGGATAACC 164
Qy 65 GCATTGAATCAGAGGGGGTTACATTAGACTTTGGAACCCCAACACAGGAGTTCGAAT 124
Db 165 GTATAGAGTCAGAGGGTGGCTTCATTAGAGACATGGGAACCCCAACAAAGCCATTCAGT 224

Qy 125 GCGCCGGCGTGGCCCTCTCTCGTTAGTCTCTCCGCCGCAACGCCCTTCGTAGCCCTTCT 184
Db 225 GTGCCGGTGTGGCCCTCTCTCGCTGCACTCAACCGCAAGCCCTTCGACAGCCTTCTCT 284
Qy 185 ACTCCAATGCTCCCGAGGAGATCTTCATCCAGCAAGGAAGGGGATACTTTTGGTGTGATAT 244
Db 285 ACACCAACGCTCCCGAGGAGATCTACATCCAACAGGTAGTGGTATTTTGGCATGATAT 344
Qy 245 TCCTGTTGTCTCTAGACACTATGAAGAGCTTCACACACAAGGTCTCGATCTCAGTCCC 304
Db 345 TCCCGGGTGTCTTAGACACATTTGAAGGCT----- 376
Qy 305 AAAGACCAACAAAGACGCTCTCAAGGAGAGACAAAGCCAAACAGCAACAGATAGTCACC 364
Db 377 -----CAACAAAAGGACAAAGCAGCAGGCCCAAGACCGTCAAC 416
Qy 365 AGNAGTGCACCGTTTCGATGAGGGTGTATCTATTCAGTTCCCAACGGGTGTGCTTCT 424
Db 417 AGAAGATCTATCACTTTCAGAGAGGGTGTATTTGATTCGAGTGCACCGTTCGATCT 476
Qy 425 GGCTCTACAACACCAACGACACTGTATGTTGCTGTTCTTCTTCTTACTGACACCAACAACA 484
Db 477 GATGTACAACAAATGAAGACACTCTCTGTTGTCGGTTCCTCTTATGACACCAACAGCT 536
Qy 485 AGCAACAACGAGCTGTATCAATTTCCCAGGAGATTTCAATTTGGCTGGGAACACGAGCAAG 544
Db 537 TCCAGAACGAGCTCGACAGATGCTTAGGATTTCTATCTGCTGGGAACCAAGAGCAAG 596
Qy 545 AGTTCTTAAGGTACACAGCAACAAAGCAGCAACAAAGCAGACGAGAGCTTTACCATATAGCC 604
Db 597 AGTTCTACAGTATACAGCCACAGACGCAAG----- 629
Qy 605 CATACAGCCGCAAGTCAAGCTAGACAAGAGAGCGTGAAATTTAGCCCTCGAGGACAGC 664
Db 630 -----GAGGTACTC 638
Qy 665 ACAGCCGACAGACGAGCAGGACAAAGAAAGAAACGAGGTGAAACATCTTCAGCG 724
Db 639 AAAGCCAGAAAGGAAAGCGTCAGCAAGAAAGAAACGAAAGGAGCAGCATATTCAGTG 698
Qy 725 GCTTACGCGGAGTCTCTGGAACAAGCCTTCAGGTTGACGACACACAGATAGTCGAA 784
Db 699 GCTTCGCCCCGAAATCTTGGAAACATGCGCTC---GTCGTGGACACGCGAGATAGTGAA 755
Qy 785 ACCTAAGAGCGCAGACCCGAGAGTGAAGAGAGAGGAGCCATTGTGACAGTGAGGGAGGCC 844
Db 756 AGCTACAGGTGAGAACGAGAGAGAGAGAGAGAGGTCCTATTGTGACAGTGAAGAGGATC 815
Qy 845 TCAGAACTTTGAGCCCGACATAGAAAGAGACGTGCCGACGAAAGAGGAATACGATGAAG 904
Db 816 TCAGCGTGATAAGCCCCACCCACGGAAGACGACCAACAAAGACCCGAGGAAGAGGAAGC 875
Qy 905 ATGAATATGAATACGATGAAGAGGATAGAAAGCGGTGGCAGGGAAGCAGAGGAGGGGA 964
Db 876 CAGATTGTGACGAGAAAGACAAACAT-----TGCCAAAGCCAAAGCAGAA 920
Qy 965 ATGCTATTCAAGAGACGATCTGACCGCAAGTGCTAAAGAAACATTTGTTAGAAACAGAT 1024
Db 921 ATGGCAATGACGAGACCATTTGCAACATGAGACTTCGCCACACATTTGCCAGACTTCAT 980
Qy 1025 CCCCTGACATCTACAACCCCTCAAGCTGGTTCACTCAAACTGCCAACGATCTCAACCTTC 1084
Db 981 CACCTGACATCTTCAACCCCTCAAGCTGGTAGCATCACAAACCGCTACCAAGCTCGACTTC 1040
Qy 1085 TAATACTTAGTGGCTTGGACCTAGTGTGATATGGAATCTCTACAGGAATGCAATCT 1144
Db 1041 CAGCCCTCTCGTGGGTCAAACTCAGTGGCCGAGTTTGGATCACTCCGCAAGAATGCTATGT 1100
Qy 1145 TTGTGCTCACTACAACACCAACGACACAGCATCATATATATGATTTGAGGGGACGGGCTC 1204
Db 1101 TGTGCCACACTACAACCTGAACGCAACAGCATATATACGATTTGAATGACGGGCAT 1160
Qy 1205 ACGTGCAAGTCTGTGGACAGCAACCGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGGTC 1264

[illegible]

Search completed: June 24, 2006, 01:56:17
Job time : 2087.24 secs

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OM nucleic - nucleic search, using sw model

Run on:	June 23, 2006, 18:21:18 ; Search time 33.1692 Seconds (without alignments)
	11014.453 Million cell updates/sec

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Perfect score: 1524
Sequence: 1 cgcacqacacccqacacqaa.....ctccagaggtcttggcttaa 1524

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 296510 segs, 119862409 residues
Total number of hits satisfying chosen parameters: 593020

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published_Applications_NA_New.*
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2: /ENC/Celerra/SIDS3/prodata/1/pubnpa/US06_NEW_PUB.seq:
3: /ENC/Celerra/SIDS3/prodata/1/pubnpa/US07_NEW_PUB.seq:
4: /ENC/Celerra/SIDS3/prodata/1/pubnpa/US08_NEW_PUB.seq:
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7: /ENC/Celerra/SIDS3/prodata/1/pubnpa/US11_NEW_PUB.seq:
8: /ENC/Celerra/SIDS3/prodata/1/pubnpa/US60_NEW_PUB.seq:
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	513	33.7	1746	6	US-10-953-349-13162	Sequence 13162, A
2	504	33.1	1711	6	US-10-953-349-13154	Sequence 13154, A
3	354.4	23.3	1247	6	US-10-953-349-21829	Sequence 21829, A
4	170.4	11.2	1768	6	US-10-449-902-7351	Sequence 7351, Ap
5	168.4	11.0	1764	6	US-10-449-902-9966	Sequence 9966, Ap
6	160.6	10.5	1586	6	US-10-449-902-9937	Sequence 9937, Ap
7	145	9.5	1655	6	US-10-449-902-9923	Sequence 9923, Ap
8	137	9.0	1650	6	US-10-449-902-9995	Sequence 9995, Ap
9	137	9.0	1667	6	US-10-449-902-9890	Sequence 9890, Ap
10	133	8.7	1654	7	US-11-284-201-4	Sequence 4, Appli
11	107.2	7.0	1796	6	US-10-449-902-7968	Sequence 7968, Ap
12	44.8	2.9	1478	6	US-10-449-902-3323	Sequence 3323, Ap
13	40.4	2.7	261789	7	US-11-260-842-1	Sequence 1, Appli
14	40.2	2.6	1364	6	US-10-449-902-152	Sequence 152, App
15	40	2.6	1632	7	US-11-217-529-76067	Sequence 76067, A
16	39.4	2.6	1632	6	US-10-953-349-10887	Sequence 10887, A
17	39	2.6	1725	6	US-10-449-902-18435	Sequence 18435, A
18	38.6	2.5	4316	6	US-10-517-441-9	Sequence 9, Appli
19	38.4	2.5	4316	6	US-10-517-441-537	Sequence 537, App
20	38.2	2.5	1987	6	US-10-449-902-28281	Sequence 28281, A
21	38.2	2.5	2185	6	US-10-449-902-6132	Sequence 6132, Ap
22	38	2.5	1977	7	US-11-217-529-647	Sequence 647, App
23	37.8	2.5	866	6	US-10-449-902-16667	Sequence 16667, A
24	37.8	2.5	1170	6	US-10-953-349-32139	Sequence 32139, A
25	37.8	2.5	1511	6	US-10-449-902-11220	Sequence 11220, A

Db	446	AGAAAGATCTATACTTCAGAGAGGGTGAATTTGATCGCAGTGCCTACTGTGTTCATGGT	505
Qy	425	GGCTCTACAACGACGACGACATGATGTGTGTCTGCTGTTCTTACTGACACCAACAACA	484
Db	506	GGATGTACAACAATGAAGACACTCCTGTGTGTCGCCGTTTCTATTATTGACACCAACAGCT	565
Qy	485	ACGACAAACAGCTTGATCAGTTCCTCCAGAGGATTCATATTTGGCTGGGAACACGGAGCAAG	544
Db	566	TGAGAAACCGAGCTCGACCGATGCTTAGGAGATTCTATCTGTCTGGGAACCAAGACCAAG	625
Qy	545	AGTTCTTAAGGTACCAGCAACAAGCAGACAAAGACGACGAAAGAGCTTACCATATAGCC	604
Db	626	AGTTTCTAAATATCAGCAAGAG-----	648
Qy	605	CATACAGCCCGCAAAAGTCAGCCTTAGACAAGAAGAGCGTGAAATTTAGCCCTCGAGGACAGC	664
Db	649	-----CAAGGAGGTCAATC	661
Qy	665	ACAGCCGACAGAAACGAGCAGGACAGAAGAAGAAACGAAAGGTGGAAACATCTTCAGCG	724
Db	662	AAAGCCGAAAGGAAGACATCAGCAAGAAGAAGAAACGAAAGGAGCGCATATTGAGTG	721
Qy	725	GCTTCACGCCGAGTTCCTGGAAACAAGCCTTCCAGGTTTGACGACACACAGATAGTGCAAA	784
Db	722	GCTTCACCTTGGAAATCTTGGAAACATGCATTGACGCT---GGACAGCAGATAGCAAAA	778
Qy	785	ACCTAAGAGCGAGACCGAGAGTGAAGAAGAGGAGGCCATTGTGAAGTGAAGGGAGGCC	844
Db	779	ACCTAAGAGAGAAACGAAGGGGAAGACAAGGAGCCATTGTGACAGATTGAAGAGGAGTTC	838
Qy	845	TCAGAACTCTGAGCCCA-----GATAGAAGAGAGCTGCGGACGAGAGAGGAAT	895
Db	839	TGAGCGTGATAAAACCAACCACCGAGCAGCAGCAACAAGACCCCGAGGAAGAAAG	898
Qy	896	ACCATGAAGATGAATA-----TGAATACGATGAAGAGGATAGAAGCGGTG	940
Db	899	AGAAGAGGATGAGAGCCACAGTGCNAGGGTAAAGCAACAACACTGCCAACGCCCGGAG	958
Qy	941	GCAGGGGAAGCAGAGGACGGGGAATGGTATTGAAGAGAGCATCTGCACGCGAAGTGCTA	1000
Db	959	GAAGCCAAAGCAAAAGCAGAAAGAAATGGCAATTGACGAGACCATATGCACCATGAGACTTC	1018
Qy	1001	AAAGAACATTTGTAGAAACAGATCCCTCAGATCTACACCCCTCAAGCTGGTTCACTCA	1060
Db	1019	GCCACAACATTTGCCAGACTTCATCATCCTGACATCTACAACCTCAAGCGCGGTAGCGTCA	1078
Qy	1061	AAACTGCCAACGATCTCAACCTTCTAATACTTAGTGGCTTGACCTAGTGTCTGAATATG	1120
Db	1079	CAACCGCCACAGCCTTGACTTCCAGCCCTCTCGTGGCTCAGCTCAGTGTGATTTG	1138
Qy	1121	GAAATCTCTACAGGAATGCAATGTTTGTGCTCACTACAACCAACGACGACACAGCATCA	1180
Db	1139	GATCTCTCCGCAAGAATGCAATGTTGTGTCACACTACACCTGAACCTGAAACGCAACAGCATAA	1198
Qy	1181	TATATCGATTTAGGGGACGGCTCAGTGCAGTCTGTGGACAGACGACGCAACAGAGTGT	1240
Db	1199	TATACGCAITTGAAATGGACGGGCATTTGATACAAGTGGTGAATTCGAACGGTGAGAGAGTGT	1258
Qy	1241	ACGACGAGGAGCTTCAAGAGGGTCACGTGCTTGTGTGGTGCACAGAACTTCGCCGTGCGTG	1300
Db	1259	TTGATGGAGAGCTGCAAGAGGGACGGGTGCTGATCGTGCCCAACAACCTTTGTGTGGCTG	1318
Qy	1301	GAAAGTCCGACGAGGAACTTCGAATACGTGGCATTCGAAGACAGACTCAAGGCCGACGA	1360
Db	1319	CAAGATCACAGAGTGACAACCTTCGAGTATGTGTCAITTCGAAGCAATGATACACCCATGA	1378
Qy	1361	TAGCAACCTCGCGGTGAAAACCTTCGCTCATAGATAACCTGCGGAGGAGGTGGTGCAG	1420
Db	1379	TCGGCACTTTGACGGGCAAACTCATTTGTGAAACGCAATTCACAGGAGAGTGAATTCAGC	1438
Qy	1421	ATTTCATATGCGCTTCCAAAGGGAGCAGGCAAGGAGCTTAAAGAAACAACCCCTTCAAGT	1480

Db	1439	ACACTTTCAACCTAAAGAGCCAGAGGCCAGGCAGAGATAAAGAACAAACACCTTTTCAAGT	1498
Qy	1481	TCCTGCTTCCACCGCTCTCAGCAGTCTCCAGAGGCTGTGGCTTA	1523
Db	1499	TCCTGCTTCCACCTCAGGAGTCTCAGAAGAGAGCTGTGGCTTA	1541
RESULT 2			
US-10-953-349-13154			
; Sequence 13154, Application US/10953349			
; Publication No. US20060107345A1			
; GENERAL INFORMATION:			
; APPLICANT: ALEXANDROV, Nikolai et al.			
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES			
; TITLE OF INVENTION: ENCODED THERBY			
; FILE REFERENCE: 2750-1579PUS2			
; CURRENT APPLICATION NUMBER: US/10/953,349			
; CURRENT FILING DATE: 2004-09-30			
; NUMBER OF SEQ ID NOS: 40252			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 13154			
; LENGTH: 1711			
; TYPE: DNA			
; ORGANISM: Glycine max			
US-10-953-349-13154			
Query Match 33.1%; Score 504; DB 6; Length 1711;			
Best Local Similarity 62.0%; Pred. No. 4,7e-146;			
Matches 943; Conservative 0; Mismatches 450; Indels 129; Gaps 4;			
Qy	5	AGCAACCCGAGAGAAACGGCTGCCAGTTCACAGCGCTCAATGCGAGAGACCTTGACAATC	64
Db	106	AGCAGCCACAGCAAAATGAGTCCAGATCCAAAAGCTGAATGCCCTCAACCGGATAACC	165
Qy	65	GCATTGAATCAGAGGGCGGTTACATTGAGACTTGGAACCCCAACCAACAGGAGTTGCAAT	124
Db	166	GTATAGAGTCGGAAGGTGGTTCATTGAGACCTTGAACCCCTAAACAAGCCATTCAGT	225
Qy	125	GGCCGGCGTCGCCCTCTCTCGTTAGTCTCTCGCGCAACGCCCTTCGTAGCCCTTCT	184
Db	226	GTGCCGGTGTGCCCTCTCTCGCTGCACCTTAAACCGCAATGCCCTTCGTAGACCTTCT	285
Qy	185	ACTCCAATCTCCCCAGGAGATCTTCATCCAGCAAGGAAGGGGATACTTTGGGTGATAT	244
Db	286	ACACCAACCGTCCCAAGAAATCTACATACACAGGTAATGGTATTTTGGCATGATAT	345
Qy	245	TCCTGGTTGTCTAGACACTATGAAGAGCTTCACACAAGGTCTCGATCTCAGTCCC	304
Db	346	TCCCGGTTGTCTTAGCACTTATCAAGAGCCGCA-----	379
Qy	305	AAAGRACCAAGACGCTCTCCAAGGAGAGACCAAGACCAACAGCAACGAGATAGTCACC	364
Db	380	-----AGAACTCTCAGAACAGAGGACGAAGCCAGAGGCCCAAGACCTTCACC	426
Qy	365	AGAAGGTGACCGCTTTTCGATGAGGGTGATCTCATTTGCAGTTCCCAACGGTGTGCTTCT	424
Db	427	AAAAGGTACATCGCTTCAGAGAGGGTGATTTGATCCAGTGCCTACTGTTGTCATGT	486
Qy	425	GGCTCTACAACGACACGACACTGATGTTGTTGCTGTTTCTCTTACTGACACCAACAACA	484
Db	487	GGATGTACAAACAATGAAGACACTCTCTGTTGTTGTCGCTTTCTATTATTGACCAACAGCT	546
Qy	485	ACGACAACAGCTTGATCAGTTCCCGAGGAGATTCAATTTGGCTGGGAACACGAGCAAG	544
Db	547	TGGAGAACAGCTTCGACCAAGATGCCCTAGAGATTTCTATCTTCTGCTGGAAACCAAGCAAG	606
Qy	545	AGTTCTTAAGGTACCAGCAACAAGACAGACAAAGACGACGAAAGAGCTTACCATATAGCC	604
Db	607	AGTTTCTAAAATATACGACGAG-----	629
Qy	605	CATACAGCCGCAAAAGTCAGCTAGCAGCAAGAAGAGCGTGAATTTAGCCCTTCGAGGACGC	664
Db	630	-----CAGCAAGGAGGTT	642

Db 900 AGAAGAGGATGAGAGCCACAGTGCAGGGTAAAGCAACACTGCCAACGCCCG 959
QY 939 TGCAGGGGAAGCAGAGCGAGGGGAATGGTATTGAAGAGACGATCTGCACCGCAAGTGC 998
Db 960 AGGAAGCCAAAGCAAAAGCAGAAGAAATGGCAITGACGAGACCATATGACCATGAGACT 1019
QY 999 TAAAAAGAACATTGGTAGAAACAGATCCCTGTGACATCTACAAACCTCAAGCTGGTTCACT 1058
Db 1020 TCGCCCAACAATTGGCCAGACATTCATCACTGACATCTCAACCCCTCAAGCCGGTAGCGT 1079
QY 1059 CAAAACTGCCAAGATCTCAACCTCTTAATTAATTAAGTGGTGGACCTAGTCTCAATA 1118
Db 1080 CACAACCGCACAGCCTTGACTTCCAGCCCTCTCGTGGCTCAGACTCAGTGTGAGTT 1139
QY 1119 TGGAAATCTCTACAGGAATGCATTGTTGTGCTCACTACAAACCAACGACACAGCAT 1178
Db 1140 TGGATCTCTCCGCAAGATGCAATGTTGCGTCCACACTCAACCTGAACCGGAACGACAT 1199
QY 1179 CATATATCGATTGAGGGGACGGCTCACGTGCAAGTCTGGACAGCAA 1226
Db 1200 AATATATGCAATTGAATGGACGGGCATTGTATACAAGTGGTGAATTGCAA 1247

RESULT 4

US-10-449-902-7351
; Sequence 7351, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7351
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK064478
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-7351

Query Match 11.2%; Score 170.4; DB 6; Length 1768;
Best Local Similarity 48.6%; Pred. No. 1.1e-42;
Matches 661; Conservative 0; Mismatches 671; Indels 28; Gaps 6;

QY 113 AGAGATTGCAATGGCGCGGCGTCCCTCTCTCGTTAGTCTCCGCGCAAGCCCTTC 172
Db 244 ATGAGTTCCGTTGTCGCGAGTGAGCGTGTAGGCGCTTAGTCTGCGAGCAAGGGCTAG 303
QY 173 GTAGGCTTTCTACTCAATGCTCCCGAGGATCTTCATCCAGCAAGGAAGGGGATCT 232
Db 304 TTTTACCAATGTATGTCTCAAGCTTGTCTACATCGTCCAAAGGTGGGGAGTGT 363
QY 233 TTGGGTGATATTCCCTGGTTGCTTAGACACTATGAAGACCTTCACACAAAGGTCGTC 292
Db 364 TTGGGATGGCACTCCCTGGTTGTC-----AGAGCGTTCCAGTCAGTTAGGT 411
QY 293 GATCTCAGTCCCAAGACACCAAGAGCTCTCCNAGAGAGAACCAAGCCACAGCAAC 352
Db 412 CTCCTTTTGAGCAAGAGGTGGCAACAGCTGGTAGGCTCAATCATCAATCCNAAAAATGA 471
QY 353 GAGATAGTACCAGAGGTGCACCGTTTCGATGAGGGTGATCTCATTTGCAAGTTCACACCG 412

Db 472 GAGACGACACAGCAACTTCCACGAGTTCACCAAGGTGATGTAATCGCAGTGCACGCTG 531
QY 413 GTGTTGCTTTTGGGCTCTACAAAGCAAGCAACACATGATGTTGTGCTGTTCTCTTACTG 472
Db 532 GAGTAGCCCACTGGCTTACATAAACAATGGTGATTCCTCTGTGGTTGCTTCACTGTCTATCG 591
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Db 592 ACACCAAGCAACAATGCCAACCAAGCTCGATCTCTAAAGAAAGGGTATGCGTACATATGCTCC 651
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Db 652 ACACAAGCATATGATATTCATATCACTATTTTGAATTTCAATGATAACAATACTCTAA 711
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QY 651 CCTCGAGGACAGCAGCGCGCAGAGAACGACGACAGCAAGAGAAAGAAACGAAGGTGG 710
Db 772 AGAAGTAGCTGGCAGCAATCGTACTCATACAGAC--AGAACAACTGAGCAGAAATCA 830
QY 711 AAACATCTTTCAGCGCTTCACGCGGAGTTCCTTGGAAACAAGCCTTCCAGTTTGACGACAG 770
Db 831 GAACTCTTTCGCTGGTTCAGCCAGATTTACTTTCTGAAGCCCTGAGTGTGAGCAAGCA 890
QY 771 ACAGATAGTGTCAAAACCTTAAGAGGCGAGACCGAGAGTGAAGAGAGGGAGCATTGTGAC 830
Db 891 AACTGTGTTGAGGCTCAAAG-----CCTGAGTGACCAAGAGGTGCCATCATTTAG 941
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Db 942 AGTTGAAATAGGCTCCAGGCACTGCGAGCCCTCTCTCAAGTTGAGCCAGTGAAGAGGA 1001
QY 891 GGAATACGATGAAGATGAATATGAATACGATGAAGAGGATAGAAG---CGTGGCAGGGG 947
Db 1002 ACNACCCCAAGCTTACTTCCCAACCAAGCAGCTACAGCCCACTGCTGTTCCGAAGTGGTG 1061
QY 948 AGCAGAGCAGGGGGAATGGTATTGAAGAGAGGATCTCCACCGCAAGTGTCTAAAAAGAA 1007
Db 1062 AGCTTGGCGGCAGCAAAATGCTCTAGATGAAATTTATGTGTGCTATTTAAGTTGAGGAAGA 1121
QY 1008 CATTTGTAGAAACAGATCCCTGACATCTACAACCTCAAGCTGGTTCACTCAAAACTGC 1067
Db 1122 CATAGACACCACAATCCAGTGACATATTAACCCCACTGGTGGAAAGATCACAGGGC 1181
QY 1068 CAACGATCTCAACCTTTCTAATCTTAGTGGCTTGGACCTAGTGTGAATATGGAATCT 1127
Db 1182 CAATAGCCAGAAATTTCCCAATACTCAATATCATCTCAGATGAGTGCACCAAGATCTCT 1241
QY 1128 CTACAGGAATGATTTGTTGCTCACTACAACACCAAGCAGCAGATCATATATCG 1187
Db 1242 CCAAAATAATAGCTTTGCTTACTCTCTATTTGGACGGTAAACGACACACCGTGTATGACGT 1301
QY 1188 ATTTGAGGACGGGCTCAGTGCAGTCTGCAAGTCTGTGACAGCAACGCGCAACAGAGTGTACGACGA 1247
Db 1302 GACCGTGGCCAAAGGCGACATCCAGTGGTGGATCACTGGTGGAGGTGCTTTGATGG 1361
QY 1248 GAGCTTCAAGAGGGTCACTGCTTGTGTGCGACAGAACTTCGCGCTCGCTGGAAGTC 1307
Db 1362 TGAGCTTCCACCAACAGCAGATCTTGTGTATCCCAAGAACTTTGCAGT--GGTGTGAAGGC 1420
QY 1308 CAGACGAGAACTTCGAATACGTGGCATTCAGACAGACTCAAGGCCAGCATAGCCAA 1367
Db 1421 TCAGCTGAAGGATTTGCAATGGGTATCTCTTCAAGACCAATCACAATGCTGTTCGACAGTCA 1480
QY 1368 CTTGCGCGGTGAAAACTCCGTCATAGATAAACCCTGCCGAGGAGGTGGTTGCAAAATTCATA 1427
Db 1481 GATCGCAGGAGGCGCTCCATTCTTCGTGCTCTACCGTTGACGTGTGCGCAATGCTTA 1540
QY 1428 TGGCTTCCAAAGGAGCAGGCAAGGCGCTTTAAGAAACAAC 1467

Db 1541 TAGGCTTCAAGGAGGACTCTAGGCATGTAAAGTTCAAC 1580

RESULT 5
US-10-449-902-9966
; Sequence 9966, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9966
; LENGTH: 1764
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107314
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9966

Query Match 11.0%; Score 168.4; DB 6; Length 1764;
Best Local Similarity 54.4%; Pred. No. 4.8e-42;
Matches 362; Conservative 0; Mismatches 301; Indels 3; Gaps 1;

QY 803 AGAGTGAAGAGGAGGAGCCATTGTGACATGAGGGAGGCCCTCAGAACTTGGAGCCAG 862
Db 790 AAAATGACCAAGAGGAGGAGAAATTTGTCGCGTTGAAACGCGGCTCAGTTTGTCTGCAACCAT 849

QY 863 ATAGAAGAGACGTGCCGCGAAGAGAGGAAATACGATGAAGATGAATATGATGATG 922
Db 850 ATGCATCTTGAAGAGCAGGAGCAAGGACAAATGCAATCAAGAGAGCATTTCAAGAAG 909

QY 923 AAGAGGATGAAGCGCTGGCAGGGGAGCAGAGGCGAGGGGAAATGGTATTGAAGAGACGA 982
Db 910 GAGGATAT---CAGCAAGTCAATATGGGAGTGGCTGCCCTAACGGTTTGGATGAGACCT 966

QY 983 TCTGCACCGCAAGTGTCTAAAGAAACATTTGGTGAAGAACAGATCCCTGACATCTACAACC 1042
Db 967 TTTGCAACCATGAGGGTAAGGCAAAACATCGATAATCCTAACCGTGTGACACATACAACC 1026

QY 1043 CTCAAGCTGGTTCACTCAAAACTGCCAAACGATCTCAACCTTCTAATCTTAGTGGCTTG 1102
Db 1027 CAAGACTGGAAGGGTTACAAATCTCAACAGCAGAAATTTCCCATTTCTTAATCTTTGATC 1086

QY 1103 GACCTAGTGTGAATATGGAATCTCTACAGGAATGCAATTTGTTCGCTCACTACAACA 1162
Db 1087 AGATGAGCGCGTTAAAGTAAATCTATACCAGAATGCACTCTCTTCAACCGTTCTGGAACA 1146

QY 1163 CGAACGCACACAGCATATATCGATTGAGGGGAGCGGCTCAGTGGCAAGTGTGAGCA 1222
Db 1147 TCAACGCTCACAGCATCGTGTATTAATCTCAAGGCGGAGCCAGGTTCAAGTTGTCAACA 1206

QY 1223 GCAACGCAACAGAGTGTACGAGAGGAGCTTCAAGAGGCTCAGTGTCTTGGTGGCCAC 1282
Db 1207 ACAATGGAAGACGGTGTCTACGAGAGGCTTCTGCGAGAGCTTCTGCGAGAGCTACTTATTTGTAAC 1266

QY 1283 AGAATCTTCGCGCTGCTGGAAAGTCCAGAGCGAGAACTTCGAATACGTGGCATTCAGA 1342
Db 1267 AACATATGTAGTTGTTAAAGAGGCAAGAGAGAGATGTGCTTACATTTGCATTCAGA 1326

QY 1343 CAGACTCAAGGCCAGCATAGCCAACTCGCCGGTGAACCTCGCTCATAGATAAACCTGCG 1402

Db 1327 CAAACCTTAACCTACTATGTAGTAAGCCACATTTGCAGGAAAGAGTTCATCTTCCTGCTCTCC 1386
QY 1403 CGGAGGAGGTGGTTGCAAAATTCATATGGCTCCAAAGGGAGCAGGCAAGCAGCTTAAGA 1462
Db 1387 CAACTGATGTTTAGCAAAATGCAATTCGATCTCAAGAGAGAGGCTCAGAGGCTCAAGC 1446
QY 1463 ACAACA 1468
Db 1447 ATAACA 1452

RESULT 6
US-10-449-902-9937
; Sequence 9937, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9937
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK107285
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-9937

Query Match 10.5%; Score 160.6; DB 6; Length 1586;
Best Local Similarity 56.8%; Pred. No. 1.2e-39;
Matches 295; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

QY 950 GCAGAGCGAGGGGAAATGGTATTGAAGAGACCATCTGCACCGCAAGTGTCTAAAAAGAAC 1009
Db 878 GAAGTGGCTGCTTAACGGTTTGGATGAGACCTTTTGACCCCTGAGGGTAAGCCAAACA 937

QY 1010 TTGGTAGAAGACAGATCCCTGACATCTACAACCTCAAGCTTCACTCAAAACTGCCA 1069
Db 938 TCGATAATCCTAACCGTGTGTATACATACAATCAAGAGCTGGAAGGGTTACAAATCTCA 997

QY 1070 ACGATCTCAACCTTCTAATCTTAGTGGCTTGGACCTAGTGTGAATATGGAATCTCT 1129
Db 998 ACACCAGAAATTTCCCATTTCTTAGTCTTGTACAGATGAGTGCAGTCAAGATTAATCTAT 1057

QY 1130 ACAGGAATGCATTTGTTGTGCTCACTACAACCAACCAACGACACAGCATCATATCGAT 1189
Db 1058 ACCAGAATGCACTCTCTTTTCCACCAATTTTGAACATCAACGCTCACACGCTCGTATATTA 1117

QY 1190 TGAGGGGAGCGGCTCAAGTGAAGTGTGGAGCAGCAACGGCAACAGAGTGTACGAGG 1249
Db 1118 CTCAAGGCGGTGCCCGGGTTCAAGTTGTCAACAACAAATGGAAGAGACAGTGTTCACGCG 1177

QY 1250 AGCTTCAAGAGAGGTCAAGTGTGGTGGCCACAGAACTTCGCGCTCGCTGGAAGTCC 1309
Db 1178 AGCTTCCGCGGAGCAGCTGCTTATATACCAACACACTATGCAGTTGTAAGAGGAC 1237

QY 1310 AGAGCGAGAACTTCGAATACGTGGCATTCAGAGCAGACTCAAGGGCCAGCATAGCAACC 1369
Db 1238 AAAGAGAGGATGTGCTTACATTTGCATTCAGACCAATCTTAATCTTATGGTAAGCCACA 1297

QY 1370 TCGCGGTGAACCTCCGCTCATAGATAACCTCGCGGAGAGGTGGTTGCAAAATTCATATG 1429

Db	1322	GACCAATGCAAACTCCATGGTGTAGCCACCTTTGAGGGGAAGAACTCAATATTTCCGTGCGAT	1381
Qy	1401	GCCGGAGGAGGTGGTTGCAAATTCATATGGCCTCCAAAGGAGCAGCAAGGAGCTTAA	1460
Db	1382	GCCAGTGGATGTGATCGCTAATGCTTACCGCATATCGAGGAGCAAGCAGCAAGCCTTAA	1441
Qy	1461	GAACAACA 1468	
Db	1442	GAATAATA 1449	
RESULT 10			
US-11-284-201-4			
; Sequence 4, Application US/11284201			
; Publication No. US20060130184A1			
; GENERAL INFORMATION:			
; APPLICANT: Abbitt, Shane E.			
; APPLICANT: Jung, Rudolf			
; TITLE OF INVENTION: Seed-Preferred Regulatory Elements			
; FILE REFERENCE: 1650			
; CURRENT APPLICATION NUMBER: US/11/284,201			
; CURRENT FILING DATE: 2005-11-21			
; PRIOR APPLICATION NUMBER: 60/634,914			
; PRIOR FILING DATE: 2004-12-10			
; NUMBER OF SEQ ID NOS: 15			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 4			
; LENGTH: 1654			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (34)...(1482)			
; OTHER INFORMATION: Leg1 coding sequence			
US-11-284-201-4			
Query Match 8.7%; Score 133; DB 7; Length 1654;			
Best Local Similarity 56.5%; Pred. No. 4.3e-31;			
Matches 247; Conservative 0; Mismatches 190; Indels 0; Gaps 0;			
Qy	1028	CTGACATCTACAAACCTCAAGCTGGTTTCACTCAAAACTGCGCAACGATCTCAACCTTCTAA	1087
Db	965	CGACGTCTACAGCCCTGGGGCTGGGAGGATCACAGCCTCACAGCACAAAGTTCCCG	1024
Qy	1088	TACTTAGTGGCTTGGACCTTAGTGTCTGAATATATGGAATCTCTACAGGAATGCATTTGTTG	1147
Db	1025	TCTCAACCTCGTACAGATCAGCGCGGTGCGGTAGACCTGTACCAGGACGCATCATGT	1084
Qy	1148	TGCTCACTACAACAACAACGACACAGCATCATATATCAATTTAGGGGACGGGCTCAGC	1207
Db	1085	CGCGTCTTGGAATTTCAACGCCACACAGCCCATGTACGGCATCAGGGGAGTGCAGAGG	1144
Qy	1208	TGCAAGTCTGGACACACACGGCAACAGAGTGTACGACGAGGAGCTTCAAGAGGTCAGC	1267
Db	1145	TCCAGTTCGCGCAGCAACCGGACCAACCGTGTTCGACGACGTCTCGTCGCGGGGAGC	1204
Qy	1268	TGCTTGTGTGCCACAGAACTTCGCGCTCGCTGGAAAGTCCCAGAGCGAGAACTTCGAAT	1327
Db	1205	TGCTCATCTACCCAGGGCTACTGTGTCACCAAGCGCGCAGGAGAGGCTTCCAGT	1264
Qy	1328	ACGTGGCATTTCAAGACAGACTCAAGGCCACAGCATATAGCAACCTTCGCGGTGAAAACTCCG	1387
Db	1265	ACATCGCTTCGAGACGAACCCCTGCACACCATGGTCAGCCACGTCTCGCGGGAAGAACTCCG	1324
Qy	1388	TCATAGATTAACCTGCGGAGGAGTGGTTGCAATTTCAATATGCCCTCCAAGGAGGAGCAGG	1447
Db	1325	TCCTGAGCACTTTCGCGCGCGCGTCACTGCGCAGCTCGTATGCGATCTCCATGGAGGAAG	1384
Qy	1448	CAAGGCAAGCTTTAAGAAC 1464	
Db	1385	CTCCAGAGCTCAAGAAC 1401	

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RESULT 11
US-10-449-902-7968
; Sequence 7968, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7968
; LENGTH: 1796
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK105316
; DATABASE ENTRY DATE: 2002-08-28
; US-10-449-902-7968

Query Match      7.0%; Score 107.2; DB 6; Length 1796;
Best Local Similarity 49.8%; Pred. No. 4.5e-23;
Matches 271; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 918 CGATGAAGAGATAGAAAGCGTGGCAGGGGAGCAGAGGCGAGGGGGAATGTTATGAAGA 977
DB 981 CGACGAGGAGATGATGAGGGGGCCCAACGCCCGCGCGCGCGGAAACGGGATCGACGA 1040

QY 978 GAGCATCTGCACCGCAAGTCTCTAAAAGAATCTGGTAGAAACAGATCCCTCGACATCTTA 1037
DB 1041 GGCCTGCTGCTTGATGAAGCTCCGCGAGAACGTCGCGGACCCCGATGAAGGCGCACCTCTA 1100

QY 1038 CAACCTCTCAAGCTGGTTTCACTCAAAATCGCAACAGATCTCAACCTTCTATATCTTAGGTG 1097
DB 1101 CACCCCAATGGCGGCGGATACCGTCTCAACAGCCAGAACGCTCCCGTCTCTCAAGCT 1160

QY 1098 GCTTGGACCTAGTCTGAATATGAAATCTCTACAGGAATGCATTTGTTTCGCTCACTA 1157
DB 1161 CATCAAGATGAGCTCAACCGCGCGTTCATGCGCGGAACGCGATCCTGCGCGCGCACTG 1220

QY 1158 CAACCAACGCAACACAGCATCATATATCGATTGAGGGGACGGGCTCACGTGCAAGTCGT 1217
DB 1221 GAACATCAACGCGACGCGCGGTGTACGCGACGAGCGGGAGCGCGAGGCTGCAGGTGGT 1280

QY 1218 GGAACAGCAACGCAACAGATGTACGACGAGGAGCTTCAAGAGGGTCACTGCTTGTGGT 1277
DB 1281 GAGCAGGAGGGGGGGGGTGTTCGACGCGAGCTCCGCGCGGGCAGATGTTGTGGT 1340

QY 1278 GCCACAGAACTTCGCCGTGCTGGAAAGTCCCAGAGCGGAACTTCGAATACGTGGCAAT 1337
DB 1341 GCCGACAGCTTCGCGTGGCGGGCGCGCGCGAGGGGTTCGCGTGGGTGCGTT 1400

QY 1338 CAGACAGACTCAAGGCCAGCATAGCCAACTTCGCGGTGAAATCTCCGTCTATAGATAA 1397
DB 1401 CCAGACGAGCGAGCGGCCATGAACGCGCGGTGGTGGCAAGTCGTCGCGCGTGC CGCG 1460

QY 1398 CTTGCGGAGAGTGGTTCAAATTCATATGCTTCAAAAGGAGGAGCAGCAAGGAGCT 1457
DB 1461 GATGCGCGGAGAGTGTCTGACAAACGCGTTTCGCGGTGTTCGAGGAGGAGCGCGCATGGT 1520

QY 1458 TAAG 1461
DB 1521 CAAG 1524
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RESULT 12
US-10-449-902-3323
; Sequence 3323, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3323
; LENGTH: 1478
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK061022
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-3323

Query Match      2.9%; Score 44.8; DB 6; Length 1478;
Best Local Similarity 51.5%; Pred. No. 0.00086;
Matches 103; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1190 TGAGGGGACGGGCTCACTCGTCAAGTGTGTGGACAGCAACGCAACAGAGTGTACGACGAG 1249
DB 871 TCGGGGGCAGCGGGCGGTGCGAGTGTGGGATCGACGGGACGCGCGTGTGGAGACCC 930

QY 1250 AGCTTCAAGAGGGTCACTGCTTGTGTGTCGCACAGAACTTCGCGCTCGTGGAAAGTCCC 1309
DB 931 GCGCCGAGGGTGGCTGCTCTTCATGTCGCCAGGTTCTTCGTGCTCTCAAGATCGCCG 990

QY 1310 AGAGCGAGAACTTCGAATACGTGGCATTCAGACAGACTCAAGGGCCAGCATAGCCAACC 1369
DB 991 AGACACCGGCGATGAGTGTCTCCATCATCACCACTCCCAACCCATCTTCTCCACC 1050

QY 1370 TCGCCGCTGAAAACTCCCGTC 1389
DB 1051 TCGCCGGGAGGACCTCCGTC 1070
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RESULT 13
US-11-260-842-1/c
; Sequence 1, Application US/11260842
; Publication No. US20060115845A1
; GENERAL INFORMATION:
; APPLICANT: Vance, Jeffrey M.
; APPLICANT: Kraus, William E.
; APPLICANT: Goldschmidt, Pascal J.
; APPLICANT: Gregory, Simon G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
; FILE REFERENCE: CARDIOVASCULAR DISEASE
; CURRENT APPLICATION NUMBER: US/11/260,842
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US 60/662,447
; PRIOR FILING DATE: 2004-10-27
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 261789
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-260-842-1
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